

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:49 : Search time 22 Seconds

(without alignments)
1712.941 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018

Sequence: 1 MDLFEDLPEDPRSPRPAK.....KAVQSGNDVYVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : PIR_73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	481	23.8	341	2	G86315 hypothetical prote
2	474	23.5	242	2	T18588 probable protein p
3	401.5	19.9	300	2	A55804 phosphoprotein pho
4	370.5	18.4	414	2	S62462 protein phosphatas
5	368	18.2	389	2	T05095 hypothetical prote
6	368	18.2	975	2	T08606 protein phosphatas
7	365	18.1	359	2	T52337 phosphoprotein pho
8	364.5	18.1	348	2	T50783 protein phosphatas
9	362	17.9	464	2	H66700 protein F12A21.5 (
10	358.5	17.8	361	2	T45778 protein phosphatas
11	353.5	17.5	355	2	H84643 probable protein p
12	352.5	17.5	434	2	T04263 phosphoprotein pho
13	352	17.4	392	2	F84650 probable protein p
14	351	17.4	404	2	T00750 probable protein p
15	350	17.3	357	2	T06308 protein phosphatas
16	348	17.2	370	2	S54297 protein phosphatas
17	347	17.2	348	2	E88434 protein F23F11.1 (
18	347	17.2	356	2	T25181 hypothetical prote
19	340	16.8	382	2	S22422 phosphoprotein pho
20	340	16.8	382	2	A32399 phosphoprotein pho
21	338.5	16.8	383	2	T48018 hypothetical prote
22	338.5	16.8	390	2	C84826 protein phosphatas
23	338.5	16.8	405	2	F86206 hypothetical prote
24	338	16.7	382	2	I53823 magnesium dependen
25	337.5	16.7	380	2	E84748 probable protein p
26	336.5	16.7	381	2	T09640 protein phosphatas
27	336.5	16.7	396	2	T02483 phosphoprotein pho
28	336	16.7	382	2	S22423 phosphoprotein pho
29	326	16.2	390	2	S65672 phosphoprotein pho

30	326	16.2	393	2	I49016 phosphoprotein pho
31	442	15.9	442	2	B86209 protein F2265.22 (
32	319	15.8	390	2	S20392 phosphoprotein pho
33	319	15.8	397	2	JC2524 phosphoprotein pho
34	317.5	15.7	281	2	S41854 phosphoprotein pho
35	309	15.3	468	2	T21331 hypothetical prote
36	307	15.2	816	2	T48123 hypothetical prote
37	306	15.2	347	2	A56058 phosphoprotein pho
38	305.5	15.1	464	2	S50592 hypothetical prote
39	305	15.1	388	2	C85323 protein phosphatas
40	302	15.0	386	2	T09019 phosphoprotein pho
41	300	14.9	491	2	T16354 hypothetical prote
42	297	14.7	423	2	T48121 hypothetical prote
43	292.5	14.5	511	2	F96732 protein phosphatas
44	289	14.3	458	2	S39832 probable phosphopr
45	284	14.1	362	2	F84695 probable protein p

ALIGNMENTS

RESULT 1

G86315

hypothetical protein T10F20.4 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: G86315

R:Theophostis. A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Comp, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, T.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Selzberg, S.L.; Schwartz, J.R.; Shum, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.K.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MIMD:21016719; PMID:11130712

A:Accession: G86315

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <STO>

A:Cross-references: GB:AE005172; NID:g9719738; PIDN:AAE97840.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match	23.8%	Score 481	DB 2	Length 341
Best local similarity	35.8%	Pred. No. 9,1e-28		
Matches 119	Conservative 66	Mismatches 107	Indels 40	Gaps 11
OY	78	KRTSPSEKNGSEELV-----EKKVCASVI-----FGLKGYVAERKGEREEMODAHYI	127	
DB	24	KAKKSEVSGGGEAAVAGNREAEEDKPSFVSEKKEFLVEADVAEDKGARHTMEDVWVY	83	
OY	128	INDITECPSPESLITRYSFAVPDGGIGIRASKFAAONLHONLIRKFPFGDYISVEKTV	187	
DB	84	LPASLDF--PGTL--KRAHFAIYDGGIGLAERKRIHLNIVNSAGLRELLDV-KVA	138	
OY	188	KRCGLDFTKHNHDEFLKASSQKPAKDGSTATCVLAUNDILYIANLQDSALICR-----	243	
DB	139	KRAILGFRKIDELQVSVS--GGWODGATACVWILLQKVFANLGDMAAVLANSTTT	196	
OY	244	---YNESSQHAALSLSKENHPTQYEEEMRTQKAGNV-RDGKVLGLVEVRSIGDQO	297	
DB	197	NELGNTEGNDLKAIVITREHKAIVPEERSIKQSGGISSNGLOGRLEVSATGDRH	256	
OY	298	YKRCGVTSVPDIRRCQTLPNDRFTLLACDGLFKVFTPEBAVFTLSCLEDEKIQTRGKS	357	
DB	257	FKKFGVSAPRDIHALETERENEMILCCDDILEVFGPSDVGAFVOKL-----KRG--	307	
OY	358	AADAREACNRLANKAV-QRGSADNVYVWV	388	
DB	308	---LHVSTVSRLVKEAVKERRCKNDCTAIVI	336	

```

RESULT 2
118588
probable protein phosphatase - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18588; T21693
R:Morimoto, B.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z18993
A:Accession: T18588
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-242 <M12>
A:Cross-references: EMBL:AL031264; PIDN:CAA20326.1; GSPDB:GN00020; CESP:F33A8.6
A:Experimental source: clone VF45EL0L
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19459
A:Accession: T21693
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-242 <M12>
A:Cross-references: EMBL:Z81525; PIDN:CAB04260.1; GSPDB:GN00020; CESP:F33A8.6
A:Experimental source: clone F33A8
C:Genetics:
A:Gene: CESP:F33A8.6
A:Map position: 2
A:Introns: 28/1; 101/1; 133/2; 202/2

Query Match      23.5%; Score 474; DB 2; Length 242;
Best Local Similarity 40.2%; Pred. No. 1.9e-27;
Matches 98; Conservative 54; Mismatches 80; Indels 12; Gaps 5;

QY 82 SEEEKNGSEELV---EKKVCASSVITGLKGYAEKRGEEEMODAHVILN--DITEBC 135
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 3 SDSRRSSDDIDNSDESKKRPESRNLYCTLAAYGCRGERADMODTHIMLPKFDLGT- 61

QY 136 RPPSLIRVSVFAVFDGHRASKFAAQNHLNLRKPR-GGVIVSEKTKRCLDIT 194
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 62 ---KSLFRASFAITFDGHAGPRAEHCOQOMGKTVKEKLAFSFPPLTSLKOTFES 118

QY 195 FKHNDDEFLKQASSOKPAWKDSTATCYLAVDNLIYANLGDRAITLCRYNEESQKHAL 254
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 119 YKAVDDGLALAKONKPIMKDOTATATMILNNVIYANIGDSRAVAVARKKEDG-SFAPV 177

QY 255 SLSEKHNPOTYEERKRIKAGGNVDGRLVGLVSRISIGDQYKRCGVTSVPDIRCOL 314
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 178 CLTYVDHDPMSHDERMIRIOKAGAVVKDGRINGVIESRSISIGDLPFKSLGIISTPDLKLTLL 237

QY 315 TPND 318
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 238 TKND 241

RESULT 3
A55804
phosphoprotein phosphatase (EC 3.1.3.16) 2c, membrane-bound - Paramaecium tetraurelia
C:Species: Paramaecium tetraurelia
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 07-Dec-1999
C:Accession: A55804
R:Klump, S.; Hanke, C.; Donella-Deana, A.; Beyer, A.; Kellner, R.; Pina, L.A.; Schultz, J. Biol. Chem. 269, 32774-32780, 1994
A:Title: A membrane-bound protein phosphatase type 2C from Paramaecium tetraurelia. Purified
A:Reference number: A55804; MUID:95105156; PMID:7806499
A:Accession: A55804
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-300 <K1U>
A:Cross-references: GB:Z36985; NID:9537421; PID:ell192609; PID:92654382
C:Genetics:
A:Genetic code: SGC5

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C:Keywords: phosphoric monoester hydrolase

Query Match      19.9%; Score 401.5; DB 2; Length 300;
Best Local Similarity 33.0%; Pred. No. 5.1e-22;
Matches 102; Conservative 53; Mismatches 105; Indels 49; Gaps 9;

QY 99 KASVITFGIKGYAEARKGEEEMODAHVILNDITECRPPSLITRVSYFAVFDGHGIR 158
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 18 QCKSVIFA---ASEMQGRNTEMDAHIRHDIID-----VSFGVFDGHCGE 63

QY 159 ASKFAAQNHLNHLI--RKPRGDVISEKTVKRCCLDTFFKHIDEFL-----KQASSOKP 211
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 64 VAQFEAKHFVDELKKNK-----EOKFEAKETFLKDELLTPEGQKEINQYXA 116

QY 212 AKND-----GSTATCYLAVDNLIYANLGDRAITLCRYNEESQKHALSLSEKHNPOTYEE 267
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 117 TPTDESIVAGCTANVALIKNTLYVANAGDSRSVLCRRNNTNH-----DKSVDHKPDNPE 170

QY 268 RMRIKAGGNVDGRLVGLVSRISIGDQYKRCG-----VTSVPDIRCOLTPNDR 319
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 171 KSRIERAGGFVSDGRVNGNLNLRALGDLEYKRDKNLSNEGLIITLAPDVKKTELTPDOK 230

QY 320 FTLLACDGLFKVFTPEAVNFTLSCLEDEKTIOTREGSAADARYEACNRLANKAVQCS 379
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 231 FTLMCDGVEFTLNHQLKQVNSTIGQAVTEELLKRAE---DLDPQLAPDTSQGTG 287

QY 380 ADNVTVNVV 388
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 288 CDNMTTILV 296

RESULT 4
S62462
protein phosphatase 2c homolog 3 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 15-Jun-2001
C:Accession: T38573; S54298; S62462
R:Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21745
A:Accession: T38573
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-414 <BAZ>
A:Cross-references: EMBL:Z54354; NID:91019398; PIDN:CAA91172.1; PID:91019405; GSPDB:G
R:Shiozaki, K.; Russell, P.
EMBO J. 14, 492-502, 1995
A:Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase
A:Reference number: S54297; MUID:95163582; PMID:7859738
A:Accession: S54298
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195, 'T', 197-414 <SHI>
A:Cross-references: EMBL:L34882; NID:9609657; PIDN:AAA67321.1; PID:9609658
C:Genetics:
A:Gene: SPAC2G11.07c
A:Map position: 1L
A:Introns: 110/1; 134/3
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match      18.4%; Score 370.5; DB 2; Length 414;
Best Local Similarity 32.9%; Pred. No. 1.5e-19;
Matches 108; Conservative 53; Mismatches 100; Indels 67; Gaps 13;

QY 81 TSEEEKNGSEELVEKKVCASSVITGLKGYAEKRGEEEMODAHVILNDITECRPPSS 140
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 10 TEKHSVNSNEP-----VLVGL-----SMQGRNTEMDAHSAI--LSMEC---SA 50

QY 141 LITKSYFAVFDGHGIRASKFAAQNHLNHLIRK--FKGDVISEKT-----VKRCCLDT 194
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 51 VKDPVDFPFAVVDGHGIRKAVKWCNSLNPQIILEKNPDFOKGDFVNLKSSFLNADAKIIDL- 109

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OY 155 FKHTDEEFLKQASSQKPMKDGSTATCVLAVDNILYIANTGDSRAILCRYNESOKHAAL 254
D 110 ----DDGFHTDPS-----GCATATVLRVNGKIKYCANAGDSRLV-----GSGKIAK 151
OY 255 SLSEKHNPTQYEEERKIRLOKAGNVRGCVLEVSRSIGDGVYKRCG-----VTSPV 307
D 152 PLSDHRRPSNEAEKARICAGFVDFGRVNGNALSRAIGDFEFKNSNLEPEKQIYATLP 211
OY 308 DIRRCOLTPNDRFILLACDGLFKVYFPEEAIVNFISLCEDEKIQTRKGSADARYEA- 366
D 212 DVVVEHTDDDEFVVLACDGLMCKTSQVIEFV-----RQIVAGTSLERIAE 260
OY 367 ---CNRLANKAVORG-SADNTVYVYVRI 390
D 261 NLMDCIASDTEETGLGCDNMVTCIVAL 288

RESULT 5
T05095
hypothetical protein F28M20.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: T05095
R:Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hohelsel, J.; Mewes,
submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15398
A:Accession: T05095
A:Molecule type: DNA
A:Residues: 1-389 <BEV>
A:Cross-references: EMBL:AL031004
A:Experimental source: cultivar Columbia; BAC clone F28M20
C:Genetics:
A:Map position: 4
A:Insertions: 95/1; 128/1; 181/1; 210/1; 274/3; 318/3
A:Note: F28M20.60
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match
Best Local Similarity 18.2%; Score 368; DB 2; Length 389;
Matches 114; Conservative 40; Mismatches 86; Indels 98; Gaps 14;

OY 109 GYAERKGEREMODAHVILNDITEECRPSSILTRVSYFAVFGHGGIRASKFAONLH 168
D 60 GY-ASSPGKRSSMEDFETRIDGVEG-----EIVGLFVGDHGGARAEEYVKONLF 110
OY 169 ONLIRKFPKGVIVSEKTVKRCILDITFKHTDEEFLKQASSQKPMKDG-STATCVLAVDN 227
D 111 SNLIR-HRK--FIS---DTTAATADAVNOTDSEFLKSEKSON---RQAGSTASTALLVGD 161
OY 228 ILVIANTGDSRAILCRYNESOKHAALSLSEKHNPTQYEEERKIRLOKAGNVR---DGRVL 284
D 162 RLIVANVGDSRAVTCRGN-----ALAVSRDHRKPDQSDERQRIEDMGGFVMAAGTWRVG 215
OY 285 GYLEVRSSTIGCGQYKRCGYVSPDIR-----ALAVSRDHRKPDQSDERQRIEDMGGFVMAAGTWRVG 310
D 216 GYLAVSRAFGDRLKQY-VVAADPEIOLVTFCONLLYIKNATLLITTEHNLHMISIVSYL 274
OY 311 -----RCQLTPNDR-----FILLACDGLFKVYFPEEAIVNFISLCEDEKIQ 351
D 275 NGLIONFLKSLISLNGKRFQEKYVDSLEFILLASDGLMDVYVNSNEAVGM-KAIEDP--- 330
OY 352 TREKGSADARYEAACNRLANKAVORGSAADNTVYVYVRI 389
D 331 -----EGAKRKLMEAYORGSADNITCVYVR 356

RESULT 6
T08606
protein phosphatase 2C-like protein Spalten - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T08606
R:Aubry, L.; Firtel, R.A.

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submitted to the EMBL Data Library, August 1997
A:Reference number: Z16434
A:Accession: T08606
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-975 <AUB>
A:Cross-references: EMBL:AF019985; NID:g2425120; PID:g2425121
A:Experimental source: strain AX3
C:Genetics:
A:Gene: spnA

Query Match
Best Local Similarity 18.2%; Score 368; DB 2; Length 975;
Matches 118; Conservative 56; Mismatches 152; Indels 80; Gaps 17;

OY 8 PEPEPSPPAAGKEAQKGPLFDLDLPPASSTDSGSGGLFDLDLPPASSGDSGLATIS 67
D 620 PKPKPEKPKPL-KPKPKPVK-ESKPKPE-----PKPKPEKPEKPEKPE 661
OY 68 QMVTTEGSKGAKRRTS-----EEKNGSEEL-----VEKKYKASVITFLKGYVAERKE 117
D 662 KEKPKTKPKPEKRTSKYDAEASKNGADSCGNGVSGSKIRLSG--FG-----SLOGR 713
OY 118 REEMODAHVILNDITEECR---PPSSILTRVSYFAVFDGNGGIRASKFAONLHONLI-- 172
D 714 RKNMDDHVLINLMGAVYINGPKDI--PISYIAVVDGCGHGETSTLLEPTVHNCIVNS 771
OY 173 RKPKPGDVIVSEKTVKRCILDITFKHTDEEFLKQASSQKPMKDGSTATCVLAVDNILYIA 232
D 772 QSFRRGD-----YEQAFRDVAVRADDIITEKE-----KSGSTGVSAALLVGNKLYTA 818
OY 233 NLGDSRAILCRYNESOKHAALS-----LSKEHNPTQYEEERKIRLOKAGNVRGCVLGYL 287
D 819 NVGDSEILVLAAPNPANPKGPVTEPVLLSKHLASDQKKRVTGLGMIIFNLFPSL 878
OY 288 EVRSISIDGQYKRR-----CGVTSVPDIRCOLTPNDRFILLACDGLFKVYFPEEAIVNFIL 342
D 879 AVSFSFGDKEKKEGKFCF--VSDPYQTTLTTFARDHFFILLACDGLMDVVEYDEAVQCV- 935
OY 343 SCLDEKIQTRKGSADARYEAACNRLANKAVORGSAADNTVYVYVRI 388
D 936 -----QKNIKLKSATK-----ISELLAQOSYDRSGSDNITVLYV 970

RESULT 7
T52337
phosphoprotein phosphatase (EC 3.1.3.16) 2C [imported] - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Mar-2002
C:Accession: T52337
R:Miyaizaki, S.; Koga, R.; Bohmert, H.J.; Fukuhara, T.
A:Title: Tissue- and environmental response-specific expression of 10 PP2C
A:Reference number: Z26045; MUID:99200489; PMID:10102366
A:Accession: T52337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <MIY>
A:Cross-references: EMBL:AF075580; PIDN:AAC36698.1
C:Genetics:
A:Gene: PP2C
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
C:Key words: phosphoric monoester hydrolase

Query Match
Best Local Similarity 18.1%; Score 365; DB 2; Length 359;
Matches 92; Conservative 59; Mismatches 94; Indels 44; Gaps 10;

OY 116 GEREMODAHVILNDITEECR---PPSSILTRVSYFAVFGHGGIRASKFAONLHONLI 169
D 58 GPKRYMDEHIIIRDLSVGLGSLFRCPRFS-----AFYVDFPGHGSAAAYVRENVMR 111
OY 170 NLIR-KFPGK---DIVISEKTVKRCILDITFKHTDEEFLKQASSQKPMKDGSTATCVLA 224

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Db 112 FFEVDVSPEASEDELEIFLE-GVENCILRRAPFLA---LALADDCSISTSSGTTALTALV 167
 225 VNDILYINILNDISRAILCRYNESQKHAALSLSEKHNPTQYEERMRIKAGGNVDGRL 284
 Db 168 LGRLLIVANMADCRVAVLCRKE-----AIDMSQDHRTYSEKRVELGCVYDDGLN 221
 285 GVLVRSRISGDOYK-----RCGVTSPDIRRCQLTPNDREFLIACDGLFKVFPPEEAVN 339
 Db 222 GVLVSRAIGDMKLPKGSASPLISEPELQIILTEDEFLICDGLMDVYISSQAVS 281
 340 FILSLEDEKIQTRGKSAADARYEACNRLANKAVQSGSADNTVMVY 388
 Db 282 IV-----RWGLKRHDDP-EQSAKDLVNEALRRHTIDNLTVIIV 318

RESULT 8

T50783
 protein phosphatase 2C-like protein - Arabidopsis thaliana
 N:Alternate names: protein T30N20_10
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Jun-2001
 C:Accession: T50783
 R:Bayan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
 submitted to the Protein Sequence Database, July 2000
 A:Reference number: 225240
 A:Accession: T50783
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <BEV>
 A:Cross-references: EMBL:AL365234
 A:Experimental source: cultivar Columbia; BAC clone T30N20
 C:Genetics:
 A:Map position: 5
 A:Introns: 27/2; 70/1; 156/1; 185/1; 209/3; 234/3
 A:Note: T30N20_10
 C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 18.1%; Score 364.5; DB 2; Length 348;
 Best Local Similarity 36.4%; Pred. No. 3.2e-19;
 Matches 103; Conservative 47; Mismatches 86; Indels 47; Gaps 13;

Qy 109 GYVAERKGEREMOD-AHYIINDITECRPPSSLITRVSYFAVFDGHCIGIRAFPAQNL 167
 Db 35 GY-ASSACKRSMEDFEFTRIDGINGELI-----VGLFGVFDGHCARAAEYVKRHL 84
 Qy 168 HQNLIRKPPKGDVSVETVRCILDTFKHDEEFLKQASSQKPAWKD-GSATCVLAVD 226
 Db 85 FSNLT-THPK--FTS--DTSATIDAYNHTDSELKSENSHN--RDAGSTASTAILVG 135
 Qy 227 NILYIANIGDSRAILCRYNESQKHAALSLSEKHNPTQYEERMRIKAGGNVDGRLV 286
 Db 136 DRLVYANNGDSRAVSRGK-----ALAVSRDKPDSDERERENMGCV--MMAGV 186
 Qy 287 LEVRSIDGQYKRCGVTSPDIRCQLTPNDREFLIACDGLFKVFPPEEAVNFTLSGLE 346
 Db 187 LAVSAFEDRLKQY-VVADEIOEIKIDTLEFLILASDGLMDVFSNEAAVAVY----- 240
 Qy 347 DEKIQTRGKSAADARYEACNRLANKAVQSGSADNTVMVY 389
 Db 241 -----KEVEDP--EDSAKKLVGEAIKRGSDNITCVVR 272

RESULT 9

H96700
 Protein F12A21.5 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96700
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cready, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maili, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tello
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96700
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-464 <STC>
 A:Cross-references: GB:AE005173; MID:911072032; PIDN:AA628911.1; GSPDB:GN00141
 A:Gene: F12A21.5
 A:Map position: 1

Query Match 17.9%; Score 362; DB 2; Length 464;
 Best Local Similarity 29.3%; Pred. No. 7.3e-19;
 Matches 108; Conservative 59; Mismatches 104; Indels 98; Gaps 13;

Qy 102 SVIFGLKGY-VAERKGEREMODAHYIINDITECRPPSSLITRVSYFAVFDGHCIGIRAS 160
 Db 113 TVSEGNFGVYVSRNGKKKMEHTRIY-----PCLVGN--KSFEGYIDHGGAKA 164
 Qy 161 KFAAONLHQNLRKPP--KGDVSVETVRCILDTFKHDEEFLKQASSQKPAWKDGT 218
 Db 165 EFVAENLHKYVVEEMENCKKEEVE-----AFKAFLRTDPRDFLEKVIKQSLKGAVSG 219
 Qy 219 ATCVIAY--DNILYIANIGDSRAILCRYNESQKHAALSLSEKHNPTQYEERMRIK 273
 Db 220 ACCVAVIYDDEMTIVSNLGDCAVLCRAG-----VAALTDHHRPGRDDEKEREISQSL 273
 Qy 274 -----AGGNVRD-----GRVLGVLVRSRISGDOYKRCGVTSPDIRRCQLTPNDREFI 321
 Db 274 IPFMFGIÖGCVVNDHOGAMKRVÖGTLAVSRISGDHLK--WVAPEPRTVLEBDMDFL 332
 Qy 322 LIACDGLKVFETPEEAVNFTLSCL-----BDEKIQ-----TREG 355
 Db 333 VLASGLMDVYVSNQAVYTVLHVAÖRTPKESEENLVÖGCVNNSPSSKLRASLTKSP 392
 Qy 356 KSADARY-----EACNRLANKAVÖRSADNV 383
 Db 393 RCANQÖSYVYNSENSPSLNREIGSSPSKSPITPKSLMAKAAÖKELANLAKRGSDMDI 452
 Qy 384 TVMVVVRIGH 392
 Db 453 TVVITIDLNH 461

RESULT 10

T45778
 protein phosphatase 2C-like protein - Arabidopsis thaliana
 N:Alternate names: protein F26013.110
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 03-Jun-2002
 C:Accession: T45778
 R:Delaney, M.; Berger, C.; Cooke, R.; Grellert, F.; Laudie, M.; Mewes, H.W.; Lemcke, K
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: 223013
 A:Accession: T45778
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361
 A:Cross-references: EMBL:AL133452
 A:Experimental source: cultivar Columbia; BAC clone F26013
 C:Genetics:
 A:Map position: 3
 A:Introns: 49/3; 108/3
 A:Note: F26013.110
 C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
 Query Match 17.8%; Score 358.5; DB 2; Length 361;
 Best Local Similarity 30.6%; Pred. No. 9.3e-19;


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QY 171 VAEKGEREEMODAHVILNDITEECRPPSSLITRVSYFAVPDGHGIRASKFAONLHON 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 LSSMOGMRASMEDAHAILDLD-----NTSFLGVYDGHGKVVSKFCAKYLLHQ 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 LI--RKFPKGDY-ISEKTVKRCLLDTFKHTDEEFLKOA-----206
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 VLSDERVAAGDVGTSLQAKFR--MDEMGGQKGMRELAVLGDKINKFSGMIEGLIWSPR 133
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 207 ---SSOKP-AM-----KDGSTATCVLAVDNILYIANIGDSRAILCRXNEESQ 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 SGDSANKPDAMAFEEGPHSDFAGPNSGSTACVAVVRDKOLEVANNAGDSRCYI-----SR 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 250 KHAALSLSKENHPQYERMRIOKAGSNVKGVLGVLEVSRTGSGOYKRCG-----302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 KNOAYMLSDHKPDLAEKERILKAGFIIHAGVNGSLMLSRIGDMEEKONKFLPSEKO 247
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 303 -VTSVPDIRCOLTPNDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAADA 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 IVTASPDVMTVELCDDDDFLVLCGDIWDCMTSOLVDFIHEQLNSE-----T 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 362 RYEAACNRLANKAVORGSA---DNVTNVR 389
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 296 KLSVCEKVLDRCLAPNTSGGEGCDNMTMILVR 328
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Search completed: January 17, 2003, 17:46:10
Job time : 25 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:46 ; Search time 14 Seconds
(without alignments)

1161.337 Million cell updates/sec

Title: US-09-935-124a-2

Perfect score: 2018
Sequence: 1 MDLFGDLPEDERSFRPAACK.....KAVGRGSDNVTVVVVRIQH 392

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401.5	19.9	300	P2C_PARTE	P49444 paramedium
2	370.5	18.4	414	P2C3_SCHPO	Q09173 schizosacch
3	359.5	17.8	454	FEM2_HUMAN	P49593 homo sapien
4	352.5	17.5	434	P2C1_ARATH	P49597 arabidopsis
5	348	17.2	370	P2C2_SCHPO	Q09172 schizosacch
6	347	17.2	356	P2C2_CAEL	P49596 caenorhabd
7	342	16.9	382	P2C1_BOVIN	O62829 bos taurus
8	341.5	16.9	450	FEM2_RAT	O9WVR7 rattus norv
9	340	16.8	382	P2C1_RABIT	P35814 onychomys
10	338	16.7	382	P2C1_RAT	O9WVR7 rattus norv
11	336	16.7	382	P2C1_MOUSE	P35813 mus musculu
12	333	16.5	423	P2C2_HUMAN	P49423 homo sapien
13	332	16.2	390	P2C1_MOUSE	O04719 arabidopsis
14	326	15.8	390	P2C1_MOUSE	P35813 mus musculu
15	317.5	15.7	281	P2C1_YEAST	P35815 rattus norv
16	317.5	15.6	387	P2C1_BOVIN	O62830 bos taurus
17	314	15.5	475	P2C1_HUMAN	O75688 homo sapien
18	313	15.2	347	P2C1_SCHPO	P49597 arabidopsis
19	306	15.1	464	P2C1_ARATH	P49596 caenorhabd
20	305.5	15.1	464	P2C1_SCHPO	P49597 arabidopsis
21	303	15.1	464	P2C1_ARATH	P49596 caenorhabd
22	300	14.9	491	P2C1_CAEL	P49596 caenorhabd
23	289	14.3	468	P2C1_YEAST	P49596 caenorhabd
24	282.5	14.0	399	P2C1_ARATH	P49596 caenorhabd
25	271.5	13.5	406	P2C1_MOUSE	O61074 mus musculu
26	269.5	13.4	542	P2C1_YEAST	P49596 caenorhabd
27	267.5	13.3	393	P2C1_YEAST	P49596 caenorhabd
28	264	13.1	449	P2C1_BOVIN	O62829 bos taurus
29	256.5	12.7	543	P2C1_HUMAN	O15355 homo sapien
30	255.5	12.7	546	P2C1_HUMAN	P49606 ustilaia ma
31	211.5	10.5	2493	P2C1_HUMAN	O15297 homo sapien
32	211	10.5	605	P2C1_HUMAN	P35816 bos taurus
33	209	10.4	538	P2C1_BOVIN	P35816 bos taurus

34	209	10.4	598	1	P2C1_MOUSE	O9G267 mus musculu
35	208	10.3	2300	1	CYAA_NEUR	O01631 neurospora
36	207	10.3	538	1	P2C1_RAT	O88483 rattus norv
37	206	10.2	1839	1	CYAA_SACCL	P23486 saccharomyc
38	204.5	10.1	383	1	P2C4_SCHPO	O14156 schizosacch
39	203	10.1	538	1	P2C1_HUMAN	O9P011 homo sapien
40	202	10.0	581	1	KAPF_ARATH	P46014 arabidopsis
41	194	9.6	529	1	P2C2_HUMAN	O9P219 homo sapien
42	189	9.3	530	1	P2C2_RAT	O88484 rattus norv
43	185.5	9.2	2026	1	CYAA_YEAST	P08678 saccharomyc
44	178	8.8	504	1	TAB1_HUMAN	O15750 homo sapien
45	178	8.8	2145	1	CYAA_PODAN	O01513 podospira a

ALIGNMENTS

RESULT 1	ID	P2C_PARTE	STANDARD	PRT	300 AA.
AC	P49444				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	Protein phosphatase 2C (PP2C).				
OS	Paramedium tetraurelia.				
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Penicillida;				
OX	NCBI_TaxID=5888;				
RN	(1)				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=51S;				
RX	MEDLINE=95105156; PubMed=7806499;				
RA	Klump S., Hanke C., Donella-Deana A., Beyer A., Kellner R.,				
RA	Pinna L.A., Schultz J.E.;				
RT	"A membrane-bound protein phosphatase type 2C from Paramedium				
RT	tetraurelia. Purification, characterization, and cloning."				
RL	J. Biol. Chem. 269:32774-32780(1994).				
CC	- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.				
CC	- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +				
CC	- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: Membrane-bound.				
CC	- PTM: THE N-TERMINUS IS BLOCKED.				
CC	- SIMILARITY: BELONGS TO THE PP2C FAMILY.				
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL: Z36985; CA85448.1; -				
DR	HSSP: P35813; IABQ.				
DR	InterPro: IPR001932; PP2C-like.				
DR	InterPro: IPR002222; PP2C.				
DR	Pfam: PF00481; PP2C; 1.				
DR	SMART: SM00331; PP2C_SIG; 1.				
DR	SMART: SM00332; PP2C; 1.				
DR	PROSITE: PS01032; PP2C; 1.				
KW	Hydrolyse; Magnesium; Manganese; Membrane.				
FT	METAL 37				
FT	METAL 38				
FT	METAL 57				
FT	METAL 237				
FT	METAL 289				
SO	SEQUENCE 300 AA; 33739 MW; BC0318BAFF7724EC CRC64;				

Query Match 19.9%; Score 401.5; DB 1; Length 300;
Best Local Similarity 33.0%; Pred. No. 7.3e-22;
Matches 102; Conservative 53; Mismatches 105; Indels 49; Gaps 9;

[illegible]

RESULT 2	PC2C_SCHPO	STANDARD:	PTT:	414 AA.
AC	PC2C_SCHPO			
AD	009173;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).			
CN	PP2C3 OR SPAC2G11.07C.			
OS	Schizosaccharomyces pombe (fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomycetes.			
OX	NCBI_TaxID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=95163582; PubMed=7859738;			
RA	Shiozaki K., Russell P.;			
RT	"Contructive role of protein phosphatase 2C (PP2C) and a MAP			
RL	kinase kinase homolog in the osmoregulation of fission yeast.";			
RL	EMBO J. 14:492-502(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=21848401; PubMed=11859360;			
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,			
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,			
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittsch E.,			
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,			
RA	Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,			
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,			
RA	Melward J., Volckaert G., Aert R., Robben J., Gryonoprez B.,			
RA	Meltdans J., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,			
RA	Borzys K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,			
RA	Eger P., Zimmermann W., Medler H., Wandut R., Purrelle B.,			
RA	Goffeau A., Cadieu E., Deyano S., Gloux S., Lelaure V., Mottier S.,			
RA	Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,			
RA	Lucas M., Rochet M., Galliard J., Tallada V.A., Garcon A., Thode G.,			
RA	Data R.R., Cruzado L., Jimenez J., Sanchez M., del Ray F., Benito J.,			

RA Dominianni A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen O., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nure P.,
 RT "the genome sequence of Schistosoma haematobium".
 RL Nature 415:871-880(2002).
 CC -I- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
 CC SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
 CC TRANSMITTED THROUGH WIS1 MAP KINASE.
 CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -I- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -I- SUBUNIT: MONOMER.
 CC -I- SIMILARITY: BELONGS TO THE PR2C FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL: L34882; AAA67321.1; -.
DR EMBL: Z54354; CAA91172.1; -.
DR HSSP: P35813; 1A60.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C_SIG; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family.
FT METAL 37 37
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 62 62 MANGANESE 1 (BY SIMILARITY).
FT METAL 230 230 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 279 279 MANGANESE 2 (BY SIMILARITY).
FT METAL 279 279 MANGANESE 2 (BY SIMILARITY).
FT CONFLICT 196 196 K -> T (IN REF. 1).
SQ SEQUENCE 414 AA; 44856 MW; EFF3416625A2B11 CRC64;

Query Match 18.48; Score 370.5; DB 1; Length 414;

Matches 108; Conservative 53; Mismatches 100; Indels 67; Gaps 13;

81 TSEEKNGSEELVEKKVCKASSVIFGLKGYVAERKGEREEMQDAHVILNDITECRPPSS 140

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b 10 TEKHSVNGSNEF-----VLYGL-----SSMQGWRISMEDAHSAI--LSMEC-----SA 50

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V 141 LITRVSYFAVEDGHGIGIRASKFAAONLHONLIRK--FPKGDVISVEKT----VKRCLLDT 194

51 YKPDVEFAYYDGHGGDKVAKWCGSNI.POTI.EKNPDFOKGFVNALKSSFLNADKAILD- 109

195 EKHTDEEEL.KOASSOKPAWKDGSTATCVI.AVDNITI.YTANI.GDSRATI.CRYNEESOKHAAT. 254

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      |::| | | | | | | | | |
DOEHTDP$-----GCTATVYI.RVGNKI.YCANAGDSPTVI-----GSKGTAK 151

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355 C1CCEUNDTQVEEBMBTQKACCMM/BDQBYI CVI EUEBETCQCCQVKBCC-----YMECVD 307

[illegible][illegible][illegible][illegible]

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RESULT 3

EMZ_HUMAN
D FEM2 HUMAN
STANDARD: PRT: 454 AA.

C: P49593; Q96PM2;

RA Wehlselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreits M., Delisny M., Puligdomenech P., Watson M., Schmidtmann T.,
RA Reichelt B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohlseil J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenhussche F.,
RA Braeken M., Melijens I., Voet M., Bastiaens I., Aert R., Delcor E.,
RA Weitzenegger T., Botne G., Ramsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirks W.,
RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Kottler P.,
RA Bergeles S., Hempel S., Feldpausch M., Lamberts S., Van den Daele H.,
RA De Keyser A., Buysbaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McMay K., Mayes R.,
RA Petzell A., Rajandream M.A., Lyne M., Benes V., Reichen T.-H.,
RA Borfova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Danner D., Herzl A.,
RA Neumann S., Argitlioni A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlin A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Scherdt F., Cooke R., Berger C., Montfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purrelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bleike C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Haeremann K.,
RA Parrell L., Dechta N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Storelle T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Mlin P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kremer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Speth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vill D., Shekier M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Chen E., Maier M., Martensen R., McComble W.R.,
RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RA thaliana";
RL Nature 402:769-777(1999).
RM [5]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shiozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RATLs) sequenced by the
RT SSP consortium (Salk/Stanford/RGC).";
RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN ABSICISIC ACID (ABA) SIGNALING PATHWAY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
CC EMBL: X78886; CAA55484.1; -;
CC EMBL: U12856; AAA50237.1; -;
CC EMBL: X77116; CAA54383.1; -;
CC EMBL: AL049448; CAB39673.1; -;
CC EMBL: AL161564; CAB79463.1; -;
CC EMBL: AY035073; AAK59578.1; -;
CC HSSP: P35813; IAO0.
CC InterPro: IPR002048; EF-hand.
CC InterPro: IPR001932; PP2C-like.

DR InterPro: IPR002022; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C-StG; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS00018; EF-HAND; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydrolyase; Magnesium; Manganese; Multigene family; Calcium-binding.
FT CA_BIND 93 104 EF-HAND (POTENTIAL).
FT DOMAIN 417 420 POLY-VAL.
FT VARIANT 180 180 G->D (MILY PHENOTYPE AND ABA-
FT CONFLICT 24 24 G->R (IN REF. 5).
FT CONFLICT 105 105 I->V (IN REF. 1).
SQ SEQUENCE 434 AA: 47505 MW: 444C54F04195F572 CRC64;
Query Match 17.5%; Score 352.5; DB 1; Length 434;
Best Local Similarity 29.4%; Pred. No. 3.9e-18;
Matches 125; Conservative 65; Mismatches 148; Indels 87; Gaps 19;
QY 2 DLFGDLPEPER-SPPRACKGAKGFLPDDLPASSTDSGGGFLPDDLPASSG
DB 45 DLMVSLPETSQSVSGSHGSESRKVLISRNPNLMKESAADIYVD-LSNG
QY 59 SCSLATSISQW-KTEGKAKKRTSEEEKNGSEELVEKVKVCASSVIFGLKGVAF
DB 101 NSDITSEKKMISRTS-----SRSLFEFK-----SVPLYGFTSIC--
QY 118 REMDQAHYLLNDIEECRPSSLI-----TRSYAFVFDGCGIRASKFAFAN
DB 138 REMEDA--VSTIPREFLOSSGSMIDGRFDPOSAAHFVGVDHGGSVAVCRF
QY 170 NLIRKPK-----GDVISEKTVKRCLLDTFKHDEEFLQASSOKPAWKDST
DB 195 ALAEELAKKPKMLCGDT-WLEKK-KKALFNSFLRVDLSIESVAPETV-----GTS
QY 223 LAVNDILTYANCDRAILCRNBSQKAHALSLSEHNPTQYEEBMRIOKAGNV-
DB 248 VVFPSSIIIFANCGDSRAVYCR-----GKTALPLSYDHRPDEDEARLEAAGKRL
QY 280 DRRVGLVEFVSRSIGDGYKRCGVTSVPDIRCQLPNRFILLCDDGLFKVFTPEAVN
DB 302 GARVGVLAAMSISGD-RILKPSIIPDEVTAVKRRKEDCLILASDGVMDVTDEACE
QY 340 FI-----LSCLEDEKIQREGKSADARVEACNRANKAVQGSADNV 383
DB 361 MARKRILLHKKKNVAVAGDSLADLER--RKEGK--DPAAMSAEYLSKLAIQRSKONI 415
QY 384 TYMNV 388
DB 416 SVVVV 420
RESULT 5
PC22_SCHPO STANDARD: PRT; 370 AA.
AC 009172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
GN PTC2 OR SPC123.11.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=95163582; PubMed=7859738;
RA Shiozaki K., Russell P.;
RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
RT kinase homolog in the osmoregulation of fission yeast.";

	Query Match	17.2%	Score 347;	DB 1;	Length 356;	
	Best Local Similarity	31.4%;	Pred. No. 7.5e-18;			
	Matches 101;	Conservative 57;	Mismatches 106;	Indels 56;	Gaps 12;	
QY	91 ELVEKKVCKASSVIFGLGYVAE---RKGEREMODAHVILNDITECRPPSSILTRVSY	147				
Db	3 OTLSEPIPTKKKSASCANENILVGSSCCMGWRVDMEDATHHLLSLDD-----PKCAF	54				
QY	148 FAVEDGHGICIRASKFAAONLHONLI--RKFKGKV--ISYEKTVKRCLLDTFKHTEDEFLK	204				
Db	55 FAVYDGHGGSVYSQSGINTLHKVVAOKFEFSGNKKAEIAEKGLE--LDQQRVREBETKD	112				
QY	205 QASSCKPAMKMGSTATCYLAVNDILYINLIGDSRAILICRYNEESQKHALSLSKENHPQ	264				
Db	113 DVS-----GTTAAVVLLIKEGDVYCGNAGSGRAVSSVGE-----ARPLSFHKRPSH	158				
QY	265 YEERMRIQKAGGNVBDGKVLGLVEVRSRISGDQYKRCG-----VTSVPDIRCOLTPR	316				
Db	159 ETEARRITIIAAGGWNVEFNRYNGNLTSLRALGDAFRAFNCDTKRAEDQIVTAFPRVITDKLPR	218				
QY	317 NDRFTLLACDGLFKVYFTPEEAVNFTLSCLEDEKIQTRREGKSAADARYEAACNRLLANKAV	375				
Db	219 DHEFTVLACDGIIMDVMTNQEVVDV-----RE-KLAERKRDPOSICBELLTRCLA	266				
QY	376 ---QRG---SADNVTVYVVRIGH	392				
Db	267 PDCQMGGLGCDNMVTVALGLDH	288				

```

RESULT 7
P2CA_BOVIN
ID P2CA_BOVIN STANDARD: PRT: 382 AA.
AC O62829;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha).
GN PP1A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=98146173; PubMed=9486768;
RA Klump S., Seike D., Fischer D., Baumann A., Mueller F., Thanos S.;
RT "Protein phosphatase type-2C Isozymes Present in Vertebrate Retinae:
RT Publication, Characterization, and Localization in Photoreceptors.";
RL J. Neurosci. Res. 51:328-338(1998).
CT 1. FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL: AJ005457; GCA06554.1; -.
DR HSSP: P35813; IABO.
DR Interpro: IPR001932; PP2C-like.
DR Interpro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C_1.
DR SMART: SM00331; PP2C_STG; 1.
DR SMART: SM00332; PP2Cg; 1.
DR

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KR	PROSITE: PS01032:	PP2C; 1.
KM	Hydrolase: Magnesium: Manganese: Multigene family	
FT	METAL	37 37 MANGANESE 1 (BY SIMILARITY).
FT	METAL	38 38 MANGANESE 1 (BY SIMILARITY).
FT	METAL	60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT	METAL	239 239 MANGANESE 2 (BY SIMILARITY).
FT	METAL	282 282 MANGANESE 2 (BY SIMILARITY).
SQ	SEQUENCE	382 AA; 42529 MW; A716B3FA0E7E21C2 CRC64;
<hr/>		
Query Match	Best Local Similarity	16.9%; Score 342; DB 1; Length 382;
Matches 101; Conservative	33.7%; Pred. No. 1.9e-17;	47; Mismatches 104; Indels 48; Gaps 12;

QY	106	GLKQYVEMRGREEMODAVILNDITIEEGRPPSILTPYSTAVFGHGCIASFAAQ	165
Db	21	GLRGCTSSMGWRVREMDAHTAVIGL-----PSGLETF-WSFAVYDGHAGSQVAKYCE	73
QY	166	NLHONLIRKRP-KGD--VISVERTVRCLLDTEKHTDEEFLKQASOKPAMKDGSTATCV	222
Db	74	HLLDHITNNODFKDSACAPSYE-NVKNGIIRTFGLFLEIDHNRYVSEKKGIGDRSGTAVGV	132
QY	223	LAVDNIILYINLGGSRALICRYNEESQKHAALSKEHNTPQYEEARRIQKAGGNVDRG	282
Db	133	LISQHTYFTINCDSRCLLR-----NRKAYPTTDHAKRSPNLEKRRIONAGGSVAIQ	166
QY	283	VLGVLEVSRISIGDQYKRC---GVT-----SVYDIRCOLTPNDRPILACDGLFK	350
Db	187	VNGSLAASRALGDGYK-CVHGKGPTEQLVSPPEVHDIRSE--EDDQFPIILACDGIWD	243
QY	331	VFFPPEAVNFLSTLE-DEKIQIRREKSAAADARYEAACNRILANKAVQSSAANNVYMY	368
Db	244	VMGNEELCDPVRKSLVETTD-----LEKVCNEVDVTCILYKSSRDMVSIVLI	289

RESULT 8			
FEM2_RAT			
ID	FEM2_RAT	STANDARD:	PRT: 450 AA.
AC	Q9WVR7		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)		
DE	(Cam-kinase phosphatase) (CamKpase).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=9279559; PubMed=10348902;		
RA	Kilanti T., Ishida A., Okuno S., Takeuchi M., Kameshita I.,		
RA	Fujisawa H.;		
RT	"Molecular cloning of Ca2+/Calmodulin-dependent protein kinase		
RT	phosphatase."		
RL	J. Biochem. 125:1022-1028(1999).		
CC	- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-		
CC	kinase II activated upon autophosphorylation, and Cam-kinases IV		
CC	and I activated upon phosphorylation by Cam-kinase kinase.		
CC	Promotes apoptosis.		
CC	- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +		
CC	phosphate.		
CC	- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).		
CC	- SUBUNIT: Associates with Flapilpha (By similarity).		
CC	- SIMILARITY: BELONGS TO THE PRKC FAMILY.		
CC	-----		
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CC EMBL: AB023634; BAA82477.1;
DR InterPro: IPR000222; PP2C
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C; 1.
DR SMART: SM00331; PP2C-Stg; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Manganese; Apoptosis; Multigene family.
FT DOMAIN 99 109 POLY-GLU.
FT METAL 356 356 MANGANESE 2 (BY SIMILARITY).
FT METAL 400 400 MANGANESE 2 (BY SIMILARITY).
SQ SSOURCE 450 AA; 49165 MW; 67626542F32B2FDD CMC64;

Query Match 16.9%; Score 341.5; DB 1; Length 450;
Best Local Similarity 29.4%; Pred. No. 2.5e-17;
Matches 124; Conservative 63; Mismatches 160; Indels 75; Gaps 16;

OY 3 LFQDLPEPSPRPAPAGKEAKGKGLFPDDLPPASSTDSGGGFLFPDDLPPASSGDSGL 62
DB LQDFPAPLPLESPPLPMK--VPGTVLQGEVEAELETFLAMGF-LGRNAPPAVA--AAVT 79
OY 63 ATSIQWVTEGKAKRKTSSEKNGSEE-----LVKK-----VCKASVY 104
DB HEATISQDLSSEKRLPEGESEEESEERVLTLDDKGLSRFFNGLMENCOSQOKR 139
OY 105 FGKGVYAEK-----GEREMODAVIINDTECRPSLITRVS-----YFA 149
DB 140 VPLTAQAPQRKLVSIHAIKTRKMKEDRVSL-----PAFNHLGLSDSVHNAIFA 191
OY 150 VFDHGIGTASKFAAONHONLIRKFKGCVISVEKTVKRCLLDTFKTDEEFLKASSO 209
DB 192 VFDHGIGVADARVASVHNTASHQ--PE-----LTDPAALKEKFRITDDMFLOKAKRE 245
OY 210 KPAWKDSTATCVLAVDNLIYANLGDRAILICRYNESOKHAALSLSEKHNPTQYEER 269
DB 246 R--LQGGTTCVCAITLGAALHVAWLGDQVYL--QOQVVKLMERKPRQDEKS 297
OY 270 RIGKAGNVR--DSRVLGVLVRSIGDQYKRCVTSVPDIRCQLTNPDRFILLACD 326
DB 298 RIALGFGVSLMDCKRWNGTGLAVSRAIG--VFQKPYVSEDAASRELTGLEDILLACD 356
OY 327 GLKFPVTPREAVNFTLSCLDEKIQTRREGKSADARYEAACRLANKAVQGSADVTVV 386
DB 357 GFEDVVRHHEIRGLVHGLLRQK--GSGMHVAE-----ELVAVARDRGSHDNITVA 405
OY 387 VV 388
DB 406 VV 407

RESULT 9
P2CA_RABIT STANDARD: PRT: 382 AA.
AC P35814;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
DE PPM1A OR PPM1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92182001; Pubmed=1311954;
RA Mann D.J., Campbell D.G., McCowan C.H., Cohen P.T.W.;
RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
RT comparative analysis of amino acid sequences."
RL Biochim. Biophys. Acta 1130:100-104(1992).
```

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CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H2O = a protein +
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: S87757; AAB21763.1;
DR PIR: S22422; S22422.
DR HSSP: P35813; 1A60.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C-Stg; 1.
DR SMART: SM00331; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 382 AA; 42462 MW; 46BC1F854FD1CA86 CRC64;

Query Match 16.8%; Score 340; DB 1; Length 382;
Best Local Similarity 33.7%; Pred. No. 2.6e-17;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

OY 106 GLKGVYAEKREEMODAHVILINDTECRPSLITRVSYPVAVDGGIGIRASKFAAQ 165
DB 21 GLRGLSLMSGWRWEMEDAHNTAVIGL-----PSGLEF--WSPFAYVDGAGSQVAKYCE 73
OY 166 NIHONLIRKFP--KGD--VISVEKTVKRCLLDTFKTDEEFLKASSQKPAWMDGSTAVCY 222
DB 74 HILDITINODPFGSAGAPSV--NVKNGIRGTGLEIDEHHRVSEKKHGADSGSTAVGV 132
OY 223 LAVDNLIYANLGDRAILICRYNESOKHAALSLSEKHNPTQYEERIRQKAGVWRDGR 282
DB 133 LISPGHTYFLINCDSRGLLCR-----NRKVHFTQDHKPSNLEKRIQNNAGSVMIQR 186
OY 283 VIGVLEVSRSIGDQYKRC-----SVDIRCQLTNPDRFILLACDGLFK 330
DB 187 VNGSLAVSRALGDPDK--CYHGKGPBOLVSPBEVDIERSE--EDDPIILLACDGLMD 243
OY 331 VFTPEAVNFTLSCLF--DEKIQTRREGKSADARYEAACRLANKAVQGSADVTVV 388
DB 244 VNGNEICDIPVRSKLEYTD-----LEKVCNEVDYDCLYGRSDNNSVILIT 289

RESULT 10
P2CA_RAT STANDARD: PRT: 382 AA.
AC P20650;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
DE PPM1A OR PPM1A OR PP2C1.
OS Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
```


RC TISSUE=Kidney; Pubmed-2538615;
 RA MEDLINE=89184515; Larner J., Fox J., Yasui A., Kikuchi K.,
 RA Tamura S., Lynch K.R., Suzuki Y., Tsukikawa S.;
 RA "Molecular cloning of rat type 2C (1A) protein phosphatase mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1796-1800(1989).
 CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC -----
 DR EMBL: J04503; AAA41917.1; -.
 DR PIR: A32399; A32399.
 DR HSSP: P35813; 1A60.
 DR InterPro: IPR001932; PP2C-like.
 DR InterPro: IPR000222; PP2C.
 DR Pfam: PF00481; PP2C; 1.
 DR SMART: SM00331; PP2C-SIG; 1.
 DR SMART: SM00332; PP2C; 1.
 DR PROSITE: PS01032; PP2C; 1.
 DR HydroLase: Magnesium; Multigene family.
 FT METAL 37 37
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 (BY SIMILARITY).
 FT METAL 239 239 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 382 AA; 42416 MW; C1C386E935374F89 CRC64;
 Query Match 16.8%; Score 340; DB 1; Length 382;
 Best Local Similarity 33.7%; Pred. No. 2,6e-17;
 Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;
 QY 106 GLKGVARKGEREMODAHYLANDITEECRPPSSLTIRVSFAVFDGHTGRASKFAAQ 165
 DB 21 GLRYGLSSMGQRMVEMDAHTAVIGL-----PSGLET-WSEFAVYDDHAGSQVAKYCE 73
 QY 166 NLHQLIRKFP--KGD--VISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGSTACV 222
 DB 74 HLHLHITNNODFKSGAGAPSV-NVKNIGIRTFLEIDEMRMVSKKKGADRSSTAVGV 132
 QY 223 LAVNLIILYANIGDSRALICRYNESOKHAALSKEHNPTQYERMRITOKAGNVNRDGR 282
 DB 133 LISPOHTFYINCGDSRGLCLR-----NRKVHFTQDHRKPSPLEKERIQAAGSVMIQR 186
 QY 283 VLGVLEVSRSIGDQYKRC---GVY-----SVPIRRCQLTPNDRFTLLACDGLFK 330
 DB 187 VNGSLAVSRALGDYK-CVHGKGPTQLVSPREVDHIERSE--EDQGFITLACDGLMD 243
 QY 331 VFTPEAVNFTLSCL--DEKIQTRREGKSADARAEACNRLANKAVORGSDANTVAVV 388
 DB 244 VMGNEELCDPVRSLRYVDD-----LEKVCNEVYDCTLYKGSRDMSVILI 289
 RESULT 11
 P2CA_MOUSE
 ID P2CA_MOUSE STANDARD: PRT: 382 AA.
 AC P4843;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (1A)
 CN (Protein phosphatase 1A).
 PPMIA OR PPMIA.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 ON NCBI_TaxID=10090;
 RX MEDLINE=94333828; Pubmed-8056349;
 RA Kato S., Kobayashi T., Terasawa T., Ohnishi M., Sasahara Y.,
 RA Kanamaru R., Tamura S.;
 RT "The cDNA sequence encoding mouse Mg2+ -dependent protein phosphatase
 alpha.";
 RL Gene 145:311-312(1994).
 CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D28117; BAA05662.1; -.
 DR HSSP: P35813; 1A60.
 DR MGD: MGI:99878; Ppmia.
 DR InterPro: IPR001932; PP2C-like.
 DR InterPro: IPR000222; PP2C.
 DR Pfam: PF00481; PP2C; 1.
 DR SMART: SM00331; PP2C-SIG; 1.
 DR SMART: SM00332; PP2C; 1.
 DR PROSITE: PS01032; PP2C; 1.
 DR HydroLase: Magnesium; Multigene family.
 FT METAL 37 37
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 (BY SIMILARITY).
 FT METAL 239 239 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 382 AA; 42432 MW; DC206610E1583870 CRC64;
 Query Match 16.7%; Score 338; DB 1; Length 382;
 Best Local Similarity 33.0%; Pred. No. 3,7e-17;
 Matches 99; Conservative 47; Mismatches 106; Indels 48; Gaps 11;
 QY 106 GLKGVARKGEREMODAHYLANDITEECRPPSSLTIRVSFAVFDGHTGRASKFAAQ 165
 DB 21 GLRYGLSSMGQRMVEMDAHTAVIGL-----PSGLET-WSEFAVYDDHAGSQVAKYCE 73
 QY 166 NLHQLIRKFP--KGDVISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGSTACV 222
 DB 74 HLHLHITNNODFKSGAGAPSV-NVKNIGIRTFLEIDEMRMVSKKKGADRSSTAVGV 132
 QY 223 LAVNLIILYANIGDSRALICRYNESOKHAALSKEHNPTQYERMRITOKAGNVNRDGR 282
 DB 133 LISPOHTFYINCGDSRGLCLR-----NRKVHFTQDHRKPSPLEKERIQAAGSVMIQR 186
 QY 283 VLGVLEVSRSIGDQYKRC---GVY-----SVPIRRCQLTPNDRFTLLACDGLFK 330
 DB 187 VNGSLAVSRALGDYK-CVHGKGPTQLVSPREVDHIERSE--EDQGFITLACDGLMD 243
 QY 331 VFTPEAVNFTLSCL--DEKIQTRREGKSADARAEACNRLANKAVORGSDANTVAVV 388
 DB 244 VMGNEELCDPVRSLRYVDD-----LEKVCNEVYDCTLYKGSRDMSVILI 289
 RESULT 12
 P2CA_HUMAN
 ID P2CA_HUMAN STANDARD: PRT: 382 AA.
 AC P4843;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (1A)
 CN (Protein phosphatase 1A).
 PPMIA OR PPMIA.


```

CC -| SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y08966; CAA70163.1; -
DR EMBL: Y08965; CAA70162.1; -
DR EMBL: Y11840; CAA72538.1; -
DR EMBL: AB024035; BAA97035.1; -
DR HSSP: P35813; 1A6Q.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C_1.
DR SMART: SM00331; PP2C-SIG; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family; Calcium-binding.
FT SEQUENCE 423 AA; 46306 MW; 67CAAC76DA531A71 CRC64;
SQ
Query Match 16.5%; Score 333; DB 1; Length 423;
Best Local Similarity 29.3%; Pred. No. 9.5e-17;
Matches 118; Conservative 63; Mismatches 130; Indels 92; Gaps 19;
OY 51 LPPAS-SDSG-----SLATISQMTVEGKGARKRSEKNSSEL----- 92
DB 34 LPSSCSGDGAMKDSFEINTQDSTLSSSSAMAGVD-----ISAGEINSGSDEFDPSS 87
OY 93 ---VKKRYCK--ASSVIFGLKGY---VAERKGEEREMOD-----AVIILND 130
DB 88 MNQSKKRLSLRRESRLFEKFCVPLCYGTSTICGRPEMEDSVSTIPRLQVSSSLDGR 147
OY 131 ITEECRPSSLLTRVSYFAVEDHGIGIRASKFAQNLH---QNLIRKFPK---GDVTSV 183
DB 148 VTNGCFPHLS---AHFGVYDGHGSGQVANCYRERHMLALTEIEVKEPECDGD--TW 201
OY 184 EKVYRCLDTFFKHTDEFELKQASQKPRAKMDGSTATCVLANDLITLANLDSRAILCR 243
DB 202 QEKMKALFNSFMVRDSELETVAHAPETV---GSTSVAAVVEPTTHIFVANCDSRAVLCR 258
OY 244 YNEESQKHAALSLSKENHPTQYEERMRIQKAGNV---RDGVLVGLVESRSIGGOYKR 300
DB 259 -----GTPPLALSYDHPKRDDEAKRIEAAQKGIYRNNGARVFGVLAHSRISGD-RYIK 311
OY 301 CGVTSVPDIRCQLTPNDRFILLACDGLFKYFTPEAVNF---IL-----SCL 345
DB 312 PSVIPPDPVTSVRVKEDDCLILASDGLMDVNTNEVCDLARKRILLMHKKNAMGELL 371
OY 346 EDEKIQTRGKSAADARIEACNRLANKAVRGSDANTVAVYV 388
DB 372 PAEK--RGEGR---DPAAMSAEYLSKMALOKSGKDNISVVV 409

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RP SEQUENCE FROM N.A.
RX MEDLINE=94099616; PubMed=8274020;
RA Terasawa T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
RA Tanaka O., Kondo H., Yamamoto H., Takeuchi T., Tamura S.;
RT "Molecular cloning of a novel isoform of Mg(2+)-dependent protein
RT phosphatase beta-4 (type 2C beta-4) enriched in brain and heart.";
RL Arch. Biochem. Biophys. 307:342-349(1993).
RN [2]
RP SEQUENCE FROM N.A. (BETA-3, BETA-4 AND BETA-5).
RC TISSUE-Testis.
RX MEDLINE=95251388; PubMed=7733667;
RA Kusuda S., Terasawa T., Kobayashi T., Ohnishi M., Sasahara Y.,
RA Kato S., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.;
RT "Molecular cloning and expression of mouse Mg(2+)-dependent protein
RT phosphatase beta-4 (type 2C beta-4).";
RL Arch. Biochem. Biophys. 318:387-393(1995).
RN [3]
RP SEQUENCE FROM N.A. (BETA-3 AND BETA-4).
RC TISSUE-Testis.
RX MEDLINE=94313028; PubMed=8038726;
RA Hou E.W., Kawai Y., Miyasaka H., Li S.S.;
RT "Molecular cloning and expression of cDNAs encoding two isoforms of
RT protein phosphatase 2C beta from mouse testis.";
RL Biochem. Mol. Biol. Int. 32:773-780(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv.
RX MEDLINE=99398339; PubMed=10469137;
RA Ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
RA Yanagawa Y., Katsura K., Hiraga A., Tamura S.;
RT "Alternative promoters direct tissue-specific expression of the mouse
RT protein phosphatase 2Cbeta gene.";
RL Eur. J. Biochem. 263:736-745(1999).
CC -| FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -| CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
CC phosphate.
CC -| COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -| SUBUNIT: MONOMER (BY SIMILARITY).
CC -| ALTERNATIVE PRODUCTS: 5 ISOFORMS, BETA-1 (SHOWN HERE), BETA-2,
CC BETA-3, BETA-4 AND BETA-5. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC THEY ONLY DIFFER IN THEIR C-TERMINUS.
CC -| TISSUE SPECIFICITY: BETA-1 IS EXPRESSED UBIQUITOUSLY; BETA-2 IS
CC EXPRESSED EXCLUSIVELY IN BRAIN AND HEART; BETA-4 IS EXPRESSED
CC EXCLUSIVELY IN BRAIN AND INTESTINE; BETA-3 AND BETA-5 ARE
CC EXPRESSED EXCLUSIVELY IN TESTIS AND INTESTINE.
CC -| SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL: D17411; BAA04233.1; -
DR EMBL: D17412; BAA04234.1; -
DR EMBL: D45859; BAA08293.1; -
DR EMBL: D45860; BAA08294.1; -
DR EMBL: D45861; BAA08295.1; -
DR EMBL: U09218; AAB60442.1; -
DR EMBL: AB007798; BAA84471.1; JOINED.
DR EMBL: AB007794; BAA84471.1; JOINED.
DR EMBL: AB007795; BAA84471.1; JOINED.
DR EMBL: AB007796; BAA84471.1; JOINED.
DR EMBL: AB007797; BAA84471.1; JOINED.
DR PIR: S39780; S39780.
DR HSSP: P35813; 1A6Q.
DR MGD: MGI:101841; Ppmlb.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C_1.
DR SMART: SM00331; PP2C-SIG; 1.

```

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SMART: SM00332: PP2C: 1.
DR PROSITE: PS01032: PP2C: 1.
KW Hydrolase; Magnesium; Manganese; Multigene family;
KW Alternative splicing
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 39 39 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
FT METAL 246 246 MANGANESE 2 (BY SIMILARITY).
FT VARSPLIC 379 390 GAGLEDSLVAL -> VSLHFPYK (IN ISOFORM BETA-2).
FT VARSPLIC 379 390 GAGLEDSLVAL -> FYOPSIASDNVFL (IN ISOFORM BETA-3).
FT VARSPLIC 379 390 GAGLEDSLVAL -> MADLSTICKPS (IN ISOFORM BETA-4).
FT VARSPLIC 388 390 VAL -> FYOPSIASDNVFL (IN ISOFORM BETA-5).
SO SEQUENCE 390 AA: 42795 MW: 255097842761899D CRC64:

Query Match 16.2%; Score 326; DB 1; Length 390;
Best Local Similarity 30.0%; Pred. No. 2,7e-16;
Matches 98; Conservative 52; Mismatches 121; Indels 56; Gaps 10;

OY 78 KRRTSEERKNGSELVEKVKASSVIFGLKGYVAERKGEREMODAHVILNDITECRP 137
DB 7 KPRTEKHNAGAGN-----GLRYGLSMQGWREMEDATAVVGI-----46
OY 138 PSSLTITRVSFAVFDGSGIRASKFAAONLHONT-----IRKPKGDVY--SVKTYKR 189
DB 47 PHGL-EDMSFFAVYDDHAGSRVANCSTHLEHTTNEDEFRADKSGFALERSVE-SVKT 104
OY 190 CLDPTFKHTDEEFLKQASSQKPAKMDGSTATCYLVANDILYIANLGDRAILCRNESCO 249
DB 105 GIRTGFLKIDYRNFSDLRNGMDRSGSVAVGMSPTHTIFNGDSRAVLCHNGO---161
OY 250 KHAALSLSKEHNPLOYEEMRIQKAGNVKRGVLYGVLEVSRTIGDGYKRCG-----302
DB 162 ---VCSFDHRCPCNPKVEKRIQNGSGSVIQRVNSLAVSALDDYKCKVDGKGPTEQ 218
OY 303 -VTSVPDIRCOLPNDREIFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRKGSADA 361
DB 219 LVSPEPEYELRAEDEFVVLACDGIWDVMSNEELCEFRVSRLE-----VSD 266
OY 362 RYEACNRLANKAVQSGADNVTVV 388
DB 267 DLENCNVVYDTCLHKGSRDMSIVLV 293

RESULT 15
P2CB-RAT STANDARD: PRT: 390 AA.
ID P2CB-RAT
AC P35815: Q64046:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (TA)
DE (Protein phosphatase 1B)
DE PPM1B OR PPM1B OR PP2C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NC NCBL_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=92201367; PubMed=1312947;
RA Henk J. J. Timmerman H.-T., Beltrich K.-G., Cohen P.-T.W., Campbell D.G.,
RT Molecular cloning and primary structure of a protein phosphatase 2C
RU isoform. 297:135-138(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;
RX MEDLINE=93169115; PubMed=7532404;
RA Schaefer K., Braun T.;
RT Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg2+
RT dependent protein phosphatase beta.
RL Biochem. Biophys. Res. Commun. 207:708-714(1995).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H2O = a protein +
CC phosphate.
CC -1- COFACTOR: BINS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms: 1/beta-1 (shown here)
CC and 2/beta-MP; are produced by alternative splicing. Isoforms
CC appear to differ in their C-terminus.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: S90449; AAB21898.1; -
DR EMBL: S74572; AAB3430.1; -
DR PIR: S20392; S20392.
DR HSSP: P35813; 1A60.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR002222; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C_Sig. 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family;
KW Alternative splicing.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
FT METAL 246 246 MANGANESE 2 (BY SIMILARITY).
FT VARSPLIC 379 390 GAGLEDSLVAL -> FYOPSPYSDNVYEMOT (IN ISOFORM 2).
SO SEQUENCE 390 AA: 42889 MW: D147615BC2FA140B CRC64:

Query Match 15.8%; Score 319; DB 1; Length 390;
Best Local Similarity 29.4%; Pred. No. 8,7e-16;
Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

OY 78 KRRTSEERKNGSELVEKVKASSVIFGLKGYVAERKGEREMODAHVILNDITECRP 137
DB 7 KPRTEKHNAGAGN-----GLRYGLSMQGWREMEDATAVVGI-----46
OY 138 PSSLTITRVSFAVFDGSGIRASKFAAONLHONT-----IRKPKGDVY--SVKTYKR 189
DB 47 PHGL-EDMSFFAVYDDHAGSRVANCSTHLEHTTNEDEFRADKSGFALERSVE-SVKT 104
OY 190 CLDPTFKHTDEEFLKQASSQKPAKMDGSTATCYLVANDILYIANLGDRAILCRNESCO 249
DB 105 GIRTGFLKIDYRNFSDLRNGMDRSGSVAVGMSPTHTIFNGDSRAVLCHNGO---161
OY 250 KHAALSLSKEHNPLOYEEMRIQKAGNVKRGVLYGVLEVSRTIGDGYKRCG-----302
DB 162 ---VCSFDHRCPCNPKVEKRIQNGSGSVIQRVNSLAVSALDDYKCKVDGKGPTEQ 218
OY 303 -VTSVPDIRCOLPNDREIFILLACDGLFKVTPPEAVNFIISLCEDEKIQTRKGSADA 361
DB 219 LVSPEPEYELRAEDEFVVLACDGIWDVMSNEELCEFRVSRLE-----VSD 266
OY 362 RYEACNRLANKAVQSGADNVTVV 388
DB 267 DLENCNVVYDTCLHKGSRDMSIVLV 293

```

Search completed: January 17, 2003, 17:44:11
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:46 ; Search time 35 Seconds

(without alignments)
2307.728 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018

Sequence: 1 MDLFGDLPPEPERSPPRPAK.....KAVRGSDNVTVMVVRIQH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriophage:*
17: SP-archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	392	4 Q9H0C8	Q9H0C8 homo sapien
2	1935	95.9	392	1 Q8R0F6	Q8R0F6 mus musculu
3	1931	95.7	392	11 Q9Z1Z6	Q9Z1Z6 rattus norv
4	1386	68.7	272	11 Q9DC99	Q9DC99 mus musculu
5	1078	53.4	212	11 Q9CS46	Q9CS46 mus musculu
6	856	42.4	167	11 Q9Z0T2	Q9Z0T2 mus musculu
7	481	23.8	341	10 Q9LMT1	Q9LMT1 arabidopsis
8	480	23.8	351	10 Q944K0	Q944K0 arabidopsis
9	474	23.5	242	5 Q62212	Q62212 caenorhabdi
10	408.5	20.2	319	10 Q8S8Z0	Q8S8Z0 mesembryant
11	398.5	19.7	311	10 Q8RXV3	Q8RXV3 arabidopsis
12	381.5	18.9	243	10 Q8S3P1	Q8S3P1 oryza sativ
13	368.5	18.3	420	10 Q8VZD9	Q8VZD9 arabidopsis
14	368	18.2	389	10 Q81773	Q81773 arabidopsis
15	368	18.2	975	5 Q15743	Q15743 dicystostei
16	366.5	18.2	420	10 Q94AT1	Q94AT1 arabidopsis

17	366.5	18.2	757	4 Q9UPP0	Q9UPP0 homo sapien
18	365	18.1	259	10 Q8Z4P9	Q8Z4P9 mesembryant
19	365	18.1	766	4 Q8WY54	Q8WY54 homo sapien
20	364.5	18.1	348	10 Q9LEW5	Q9LEW5 arabidopsis
21	364.5	18.1	371	10 Q8VFN9	Q8VFN9 arabidopsis
22	362	17.9	464	10 Q9FXE4	Q9FXE4 arabidopsis
23	361	17.9	380	10 Q8RX37	Q8RX37 arabidopsis
24	359.5	17.8	454	4 Q96PM2	Q96PM2 homo sapien
25	358.5	17.8	361	10 Q9SD02	Q9SD02 arabidopsis
26	355.5	17.5	355	10 Q81716	Q81716 arabidopsis
27	353.5	17.5	362	10 Q9ZPE9	Q9ZPE9 lotus japon
28	352	17.4	307	10 Q9FCM3	Q9FCM3 arabidopsis
29	352	17.4	392	10 Q9SLA1	Q9SLA1 arabidopsis
30	351	17.4	404	10 Q22200	Q22200 arabidopsis
31	351	17.4	658	10 Q940A2	Q940A2 arabidopsis
32	350	17.3	305	10 Q942N4	Q942N4 oryza sativ
33	350	17.3	357	10 Q9S253	Q9S253 arabidopsis
34	341.5	16.9	450	11 Q9WV77	Q9WV77 rattus norv
35	339	16.8	383	10 Q9LP12	Q9LP12 arabidopsis
36	338.5	16.8	396	10 Q9M1P8	Q9M1P8 arabidopsis
37	338.5	16.8	390	10 Q8XEE8	Q8XEE8 arabidopsis
38	338.5	16.8	405	10 Q9LMK9	Q9LMK9 arabidopsis
39	338	16.7	323	11 Q9EDZ2	Q9EDZ2 mus musculu
40	338	16.7	326	11 Q9EDZ3	Q9EDZ3 mus musculu
41	338	16.7	326	11 Q8R4T7	Q8R4T7 mus musculu
42	337.5	16.7	380	10 Q8Z4F8	Q8Z4F8 mesembryant
43	337.5	16.7	380	10 P93006	P93006 medicago sa
44	336.5	16.7	381	10 Q24078	Q24078 medicago sa
45	336.5	16.7	396	10 Q80871	Q80871 arabidopsis

ALIGNMENTS

RESULT 1
Q9H0C8 PRELIMINARY; PRT; 392 AA.
ID Q9H0C8
AC Q9H0C8
DT 01-MAR-2001 (TREMURel. 16, Created)
DT 01-MAR-2001 (TREMURel. 16, last sequence update)
DT 01-MAR-2002 (TREMURel. 20, last annotation update)
DE Hypothetical 42.9 kDa protein (Integrin-linked kinase-associated
DE serine/threonine phosphatase 2C).
GN DKPZP434J2031
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Leung-Hagesleijn C., Mewes H.W., Weil B., Wiemann S.;
RT 'Modulation of integrin signal transduction by ILKAP, a protein
RL phosphatase 2C associating with the integrin-linked kinase, ILK1'.
RN EMBO J. 0:0-0(2001).
[3]
RP SEQUENCE FROM N.A.
RA Strusberg R.;
RT TISSUE-UTERUS;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL136850; CAB66784.1; -;
DR EMBL: AY024365; AA00736.1; -;
DR EMBL: BC006576; AA006576.1; -;
DR HSSP: P35813; 1A60.
DR InterPro: IPR000222; PPTC.
DR InterPro: IPR001932; PPTC-like.
DR Pfam: PF00481; PPTC; 1.
DR SMART: SM00352; PPTC; 1.
DR SMART: SM00351; PPTC_Sig; 1.

DR PROSITE: PS01032; PP2C; 1.
KW Hypothetical protein; Kinase.
SQ SEQUENCE 392 AA; 42906 MW; AF6ACC98508CBEA3 CRC64;

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 4,4e-156;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPDDLPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPDDLPASSGDSG 60
OY 61 STATSIQWVKTEGKAGKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
DB 61 STATSIQWVKTEGKAGKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
OY 121 MODAVHILNDITIEECRPSSLTTRVSYFAVPDGHGIRASKRAAONLHONLIRKPKGV 180
DB 121 MODAVHILNDITIEECRPSSLTTRVSYFAVPDGHGIRASKRAAONLHONLIRKPKGV 180
OY 181 ISEKTVKRCCLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGSRAI 240
DB 181 ISEKTVKRCCLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGSRAI 240
OY 241 LCRYNESQKHAALSLSKHNPTQYEERMRIQAGGNVBDGVLGVLEYSRSIGDQYKR 300
DB 241 LCRYNESQKHAALSLSKHNPTQYEERMRIQAGGNVBDGVLGVLEYSRSIGDQYKR 300
OY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFILSCLEDEKIQTRREGSAAD 360
DB 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFILSCLEDEKIQTRREGSAAD 360
OY 361 ARYEACNRLANKAVQSGADNVTVWVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVWVRIGH 392
```

RESULT 2

08R0F6 PRELIMINARY; PRT; 392 AA.
AC 08R0F6:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to protein phosphatase 2C.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026953; AAH26953.1; -
SQ SEQUENCE 392 AA; 42774 MW; 8DE1F77DAC987176 CRC64;

Query Match 95.9%; Score 1935; DB 11; Length 392;
Best Local Similarity 95.2%; Pred. No. 2.5e-149;
Matches 373; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

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OY 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPDDLPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPDDLPASSGDSG 60
OY 61 STATSIQWVKTEGKAGKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
DB 61 STATSIQWVKTEGKAGKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
OY 121 MODAVHILNDITIEECRPSSLTTRVSYFAVPDGHGIRASKRAAONLHONLIRKPKGV 180
DB 121 MODAVHILNDITIEECRPSSLTTRVSYFAVPDGHGIRASKRAAONLHONLIRKPKGV 180
```

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OY 181 ISEKTVKRCCLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGSRAI 240
DB 181 ISEKTVKRCCLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGSRAI 240
OY 241 LCRYNESQKHAALSLSKHNPTQYEERMRIQAGGNVBDGVLGVLEYSRSIGDQYKR 300
DB 241 LCRYNESQKHAALSLSKHNPTQYEERMRIQAGGNVBDGVLGVLEYSRSIGDQYKR 300
OY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFILSCLEDEKIQTRREGSAAD 360
DB 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFILSCLEDEKIQTRREGSAAD 360
OY 361 ARYEACNRLANKAVQSGADNVTVWVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVWVRIGH 392
```

RESULT 3

092126 PRELIMINARY; PRT; 392 AA.
AC 092126:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein phosphatase 2C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99074314; PubMed=9857069;
RA Tong Y., Quirion R., Shen S.H.;
RT "Cloning and characterization of a novel mammalian PP2C isozyme."
RL J. Biol. Chem. 273:35282-35290(1998).
DR EMBL; AF095927; AAC97497.1; -.
DR HSSP; P35813; IAOQ.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C-SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 392 AA; 42744 MW; 1468FDE0BA60D915 CRC64;

Query Match 95.7%; Score 1931; DB 11; Length 392;
Best Local Similarity 95.2%; Pred. No. 5.3e-149;
Matches 373; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

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OY 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPDDLPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPDDLPASSGDSG 60
OY 61 STATSIQWVKTEGKAGKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
DB 61 STATSIQWVKTEGKAGKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
OY 121 MODAVHILNDITIEECRPSSLTTRVSYFAVPDGHGIRASKRAAONLHONLIRKPKGV 180
DB 121 MODAVHILNDITIEECRPSSLTTRVSYFAVPDGHGIRASKRAAONLHONLIRKPKGV 180
OY 181 ISEKTVKRCCLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGSRAI 240
DB 181 ISEKTVKRCCLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGSRAI 240
OY 241 LCRYNESQKHAALSLSKHNPTQYEERMRIQAGGNVBDGVLGVLEYSRSIGDQYKR 300
DB 241 LCRYNESQKHAALSLSKHNPTQYEERMRIQAGGNVBDGVLGVLEYSRSIGDQYKR 300
OY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFILSCLEDEKIQTRREGSAAD 360
DB 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFILSCLEDEKIQTRREGSAAD 360
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Oy		361 ARFEACNRANKAVGSGADNTWYVRICH	392
Dd		361 ARFEACNRANKAVGSGADNTWYVRICH	392
RESULT 4			
ID	Q9DC99;	PRELIMINARY;	PRT; 272 AA.
AC	Q9DC99;		
DT	01-JUN-2001 (TREMBLrel, 17, Created)		
DT	01-JUN-2001 (TREMBLrel, 17, Last sequence update)		
DE	01-MAR-2002 (TREMBLrel, 20, Last annotation update)		
DE	0710007ALARIK protein.		
GN	0710007ALARIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;		
OC	Emmalyota; Euterbia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SRRAIN-C57BL/6J; TISSUE-BRAIN:		
RX	MEDLINE=21085660; PubMed=112117851.		
RA	Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Akaiwa T., Hara A., Fukunishi Y., Komio H., Adachi J., Furuta S.,		
RA	Alizawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamahata I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasakawa T., Saito R.,		
RA	Kodora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,		
RA	Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schirni L.M., Stuhli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Futuno M., Anno H., Baldarelli R., Barsh G.,		
RA	Blaize J., Boftelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofman M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyon P., Marchionni L., Mashima J., Mazzarelli J., Mombearts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection";		
RL	Nature 409:685-690(2001).;		
DR	EMBL: AK003007; BAB22508.1; -;		
DR	HSSP: P35813; 1A6O		
DR	MCD; MGI:1914694; 0710007ALARIK.		
DR	InterPro: IPRO00222; PP2C-like.		
DR	InterPro: IPRO01932; PP2C-like.		
DR	Pfam: PF00481; PP2C; 1.		
DR	SMART: SM00332; PP2Cc; 1.		
DR	SMART: SM00331; PP2C-STG; 1.		
DR	PROSITE: PS01032; PP2C; 1.		
SO	SEQUENCE 272 AA; 30279 MW; 485F2959D91BA63D CRC64;		
Query Match			
Best Local Similarity	98.7%; Score 1386; DB 11; Length 272;		
Matches 266; Conservative 3; Mismatches 3; Indels 0; Gaps 0;			
Oy	121 MOAHYTLNDITEECRPPSSLITRVSYVAFPGHGIGIRASKFAEONJHNLIRPKPKDY 180		
Dd	1 MOAHYTLNDITQECNPSSLITRVSYFAVFDDGGHIGIRASFEANQNHLNLRPKPKDI 60		
Oy	181 ISYEKYVXCILIDFKRHDPDEFLLKQASSOKPAWKGSATVCVALAVNIILYINLGDSAI 240		
Dd	61 ISYEKVTKCLIDFTKRHDDEFLLKQASSOPAKMKGSATVCVALAVNIILYINLGDSAI 120		
Oy	241 LCRIINESOKHAALSLSKEAHNPYOYERRMRICAGAGNRDGRVLGYEVSRISIGGCYKR 300		
Dd	121 LCRIINESOKHAALSLSKEAHNPYOYERRMRICAGAGNRDGRVLGYEVSRISIGGCYKR 180		
Oy	301 CGVTSVPDIRRCQLTPNDRTLLAACDGLRKVFPEEAVNFLTSLCLEDEKLTGRECKSAAD 360		
Dd	181 CGVTSVPDIRRCQLTPNDRTLLAACDGLRKVFPEEAVNFLTSLCLEDEKLTGRECKSPVD 240		

QY	361	AREEACNR	LANKAV	RGSGADNT	YAWVR	RIH	392
DB	241	AREEACNR <td>LANKAV<td>RGSGADNT<td>YAWVR<td>RIH</td><td>272</td></td></td></td>	LANKAV <td>RGSGADNT<td>YAWVR<td>RIH</td><td>272</td></td></td>	RGSGADNT <td>YAWVR<td>RIH</td><td>272</td></td>	YAWVR <td>RIH</td> <td>272</td>	RIH	272
RESULT	5						
Q9CS46							
ID	Q9CS46	PRELIMINARY		PRY		212	AA
AC	Q9CS46						
DT	01-JUN-2001	(TREMBLrel. 17, Created)					
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)					
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)					
DE	0710007A14R1K	protein (Fragment).					
OS	0710007A14R1K						
GN	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_Taxid:10090;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	SRRAIN-C57BL/6J; TISSUE-EMBRYO;						
RX	Medline:12085660; PubMed:11217851;						
RA	Kawai J, Shingaga A., Shibata K., Yoshino M., Itoh M., Ishii Y.,						
RA	Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,						
RA	Alzawa K., Izawa M., Nishi K., Kiyosaka H., Kondo S., Yamanaka I.,						
RA	Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,						
RA	Kadota K., Matsuda A.A., Ashdunet M., Batalov S., Casavant T.,						
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,						
RA	Knehl P., Lewis S., Matsuo T., Nkaioto I., Pesole G., Quackenbush J.,						
RA	Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,						
RA	Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barish G.,						
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,						
RA	Brominstein M.J., Bult C., Fletcher C., Fujita A., Kamiya M., Lee N.H.,						
RA	Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombaerts P.,						
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,						
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,						
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,						
RA	Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kotsuki S.,						
RA	Hayashizaki Y.;						
RT	"Functional annotation of a full-length mouse cDNA collection.";						
RL	Nature 409:685-690(2001).						
DR	EMBL: AK019158; BAB31574.1; -						
DR	HSSP: P35813; IAG0.						
DR	MED: MG1:1914694; 0710007A14R1K.						
DR	InterPro: IPR001932; PP2C-like.						
DR	Pfam: PF00481; PP2C_1.						
DR	SMART: SM00332; PP2C_1.						
FT	NON_LINER						
SO	SEQUENCE	212	AA:	23615	MM:	133286D628B540D7	CRC64:
	Query Match	53.4%	Score 1078:	DB 11:	Length 212:		
	Best Local Similarity	96.1%:	Pred. No. 6:	je-80:			
	Matches 208:	Conservative 2:	Mismatches 2:	Indels 0:	Gaps 0:		
QY	181	ISEKTVKSCLLDPTFKATDEEFILKQAS	SOKPAMKDGSTATCVALVNDILYANLGDSSAI	240			
DB	1	ISEKTVKSCLLDPTFKATDEEFILKQAS	SOKPAMKDGSTATCVALVNDILYANLGDSSAI	60			
QY	241	LCRRNESQKHAALSLSKENHPQCYEEBRRIRIKACAGNROGRLVGLVEYSRISIGDGYK	300				
DB	61	LCRRNESQKHAALSLSKENHPQCYEEBRRIRIKACAGNROGRLVGLVEYSRISIGDGYK	120				
QY	301	CGATSPDRIKCOLPNDRFILACGCEKRYTPEEAVANFLISLDEDEKIQREKSSAD	360				
DB	121	CGATSPDRIKCOLPNDRFILACGCEKRYTPEEAVANFLISLDEDEKIQREKSSAD	180				
QY	361	ARFEACNRLANKAVRGSGADNTYAWVR	RIH 392				
DB	181	ARFEACNRLANKAVRGSGADNTYAWVR	RIH 272				

0920T2 PRELIMINARY: PRT: 167 AA.
ID 0920T2
AC 0920T2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 18.8 kDa protein (Fragment).
GN 071007A14RLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Stohard P.M., Pillgrim D.;
RL "Isolation of PP2C sequences using degenerate-oligo PCR."
DR EMBL: AF117831; AAD17234.1; -.
DR HSSP: P35813; IAGO.
DR MGD: MGI:1914694; 071007A14RLK.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
KW Hypothetical protein.
FT NON_TER 1
FT 167
SQ SEQUENCE 167 AA; 18795 MW; 3A4FC2F809DD95B CRC64;
Query Match 42.4%; Score 856; DB 11; Length 167;
Best Local Similarity 98.8%; Pred. No. 5.1e-62;
Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 157 TRASKFAONLQNTIRKPKGDVTSVEKTVKRCCLIDPFKHTDEFLKASSOKPAWKKG 216
DB 1 TRASKLAONLQNLIRKPKGDITISVEKTVKRCCLIDPFKHTDEFLKASSOKPAWKKG 60
QY 217 STATCVLAVDNILYIANLGDSTRALICRYNEESQKHAALSLSEHNPTQYEEMRIQKAG 276
DB 61 STATCVLAVDNILYIANLGDSTRALICRYNEESQKHAALSLSEHNPTQYEEMRIQKAG 120
QY 277 NVRDGRVLCVLEVSIGDGQYKRCGVSVPIRRCQLTPNDRFILL 323
DB 121 NVRDGRVLCVLEVSIGDGQYKRCGVSVPIRRCQLTPNDRFILL 167
RESULT 7
09LMT1 PRELIMINARY: PRT: 341 AA.
ID 09LMT1
AC 09LMT1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE T10F20.4 protein.
GN T10F20.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
RA Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
RA Federgrain N.A., Theologis A.;
RL "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1.";
DR Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC034107; AAF97840.1; -.
DR HSSP: P35813; IAGO.

DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00331; PP2C-SIG; 1.
SQ SEQUENCE 341 AA; 37367 MW; 6873C0CEB2310195 CRC64;
Query Match 23.8%; Score 481; DB 10; Length 341;
Best Local Similarity 35.8%; Pred. No. 4.9e-31;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;
QY 78 KRKTSSEKNGSEELY-----EKVKCKASSVT-----FGLKGYVAREKREEMODAHVI 127
DB 24 KAKKSEEVSGGEEAANAAGNRREAEDEKPSFVSEKKEFLVEADVADKARHTMEDVWVY 83
QY 128 LNDITEECRPPSSILTRVYFAVDFGHSIRSKFAONLQNLIRKPKGVISVEKTV 187
DB 84 LFDASIDF--PCTL--KCHFAITDGGRLAEFAKKLHLNLSAGLPRELLDV-KVA 138
QY 188 KRCLDTEFKHTDEEFLKQASOKPAWKDSTATCVLAVDNILYIANLGDSTRALICR---- 243
DB 139 KKAILEGFRKTDDELLQKSVS--GGWQDGAFAVCWILDQKFFVANIGDAKAVLARSTT 196
QY 244 -----YNEESQKHAALSLSEHNPTQYEEMRIQKAGNV-RDGRVLCVLEVSIGDGQ 297
DB 197 NELGNHTEAGNPLKAIVLREKKAITYPOERSRIQSGGVISNGRLOGRLVSRFAFGDH 256
QY 298 YKRCGVTSVPDRIKRCQLTPNDRFILLACDGLFKVFPPEAVNFILSCLEDEKIQTRKGS 357
DB 257 FKFGVSAITPDIAHELTERENFMILGCDLWEVGPSPDAVGFVKLL-----KEG-- 307
QY 358 AADAREAAACNLANKAV-QRGSADNVTVWVY 388
DB 308 ---LHVSTVSRLVKEAVEKERCNDCTAIVI 336
RESULT 8
0944K0 PRELIMINARY: PRT: 351 AA.
ID 0944K0
AC 0944K0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE A1918030/T10F20_3.
GN A1918030.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Katlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL "Arabidopsis cDNA clones."
DR Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF428352; AAL16282.1; -.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
SQ SEQUENCE 351 AA; 38514 MW; AFE224E0EE003229 CRC64;
Query Match 23.8%; Score 480; DB 10; Length 351;
Best Local Similarity 35.8%; Pred. No. 6.1e-31;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;
QY 78 KRKTSSEKNGSEELY-----EKVKCKASSVT-----FGLKGYVAREKREEMODAHVI 127
DB 34 KAKKSEEVSGGEEAANAAGNRREAEDEKPSFVSEKKEFLVEADVADKARHTMEDVWVY 93

[illegible]

KM Hypothetical protein.
SQ SEQUENCE 243 AA; 26734 MW; 8B481E1F555CE5F CRC64;

Query Match 18.9%; Score 381.5; DB 10; Length 243;
Best Local Similarity 37.9%; Pred. No. 3,8e-23;
Matches 96; Conservative 43; Mismatches 75; Indels 39; Gaps 7;

QY 145 VSYNAVFDHGCIASAKFAAONLHONILR--KFKRGDIVSEKYVKRCRLDLPFKHTDEEF 202
:
Db 17 IGLFEVDDGHEGAVAAEVKKONLFSLHRHPKFISDTKVAID-----DAYSTDSDF 68
:
QY 203 LKAQSSOKPAKDGSTATCAVLADNIIYLIALMGSRALICRYNEESOKHAALSKEHN 262
:
Db 69 LESSSONQC---GSTASTAVLVGDRLFVANVGDSRALTCGN-----ALAASKDHKP 119
:
QY 263 TQVERMRRIQKAGNVNR--DGRVLGVLEVSRTIGDGOYKRGGTYSVPDIRCOLTPMDR 319
:
Db 120 DQTEBERORIEDACGFVMWAGTVAGCVLAVRAGDKLKQYVVVD--PEIREEVHDLSLE 178
:
QY 320 FILLACGLEVFVTFPEEVANFTLSCLDEEKIQTRNGKAAARVEAACNLANKNAVGS 379
:
Db 179 FLIIASOGMLOVVINEEAVDFTSRIDPEE-----AAKKLLQEAHKRES 222
:
QY 380 ADNTVAVWRIGH 392
:
Db 223 SDNITCIVVRELH 235

RESULT 13
08VZD9 PRELIMINARY; PRT; 420 AA.

AC 08VZD9;
DT 01-MAR-2002 (TREMBLrel_20, Created)
DT 01-MAR-2002 (TREMBLrel_20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel_21, Last annotation update)
DE AT5G53140/MFH8.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucostrids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cdna clones";
RL submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY065026; AAL57666.1; -
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2CC; 1.
DR SMART: SM00331; PP2C_SIG; 1.
DR PROSITE: PS01032; PP2C; UNKNOWN.1.
SO SEQUENCE 420 AA; 45752 MW; ZDF6960D75BF9058 CRC64;

Query Match 18.3%; Score 368.5; DB 10; Length 420;
Best Local Similarity 32.8%; Pred. No. 9.5e-22;
Matches 112; Conservative 60; Mismatches 108; Indels 61; Gaps 13;

QY 64 TSISOMVTEBGKARKRKTSBEERKNSSELVEKKVCASSVIFGLK-----GIYAERK 115
:
Db 58 TSAKMAMVT-----SAGEKRISLVMPPEKVDGCGYGGMWNDDGSLSCGYCSFR- 108
:
QY 116 GEREMOAHYIANDITEECRRPSSLIRVSFYAFNDHGGRASKFAAONLHOUNLRKF 175
:
Db 109 GKRMTEPFQFIKASTICG-----QAVCFEGFLFDGHGSGRAEYVLEKHLENLNM-KH 159
: :

```

QY 176 PKGDVLSVEKTVKRCLLDTPFKHTDEFLKQASOKPAMK-DGSTATCVLAVDNILYIANL 234
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 160 PQ-----FLDTFKLALNTETVQDVALE-----SEKQTYRNDOSFASAAVLGNHLYAVN 211
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 235 GDSRATLCYNEESOKHAALSLSKEHNPQYERMRIOKAGNVR---DGRVIGYLEVSR 291
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 212 GDSRTIV-----SKACALALSDHRCFNRSDERKRKISAGSVIMAGTMRVGGVLAWSR 265
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 292 SIGDQYKRCGYTSVPDIRRCQLTPNDRIPLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 266 ALGNRMRLKQF-VVAPELEIODELEIDHEALLIVLASDGLMDVYVNEAV--ALAOSEEP-- 320
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 352 TREGKSADARYEAACNRLANKAVORGSDADNTVAVVIRGH 392
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 321 -----EAAARKLDTAFSRGSDADNITICIVKFRH 349
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 14
ID 081773 PRELIMINARY; PRT; 389 AA.
AC 081773;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 42.6 kDa protein.
GN F28M20.60 OR AT4G31750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Hohnsels J.,
RA Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;
RU Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RU Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RU Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031004; CA19748.1; -.
DR EMBL; AL161579; CAB79893.1; -.
DR HSSP; P35813; IAG0.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C.1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C-StG; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOMN_1.
DR PROSITE; PS01032; PP2C; 1.
KW Hypothetical protein
SQ SEQUENCE 389 AA; 42562 MW; A7C4C39764ECLDEA CRC64;

Query Match 18.2%; Score 368; DB 10; Length 389;
Best Local Similarity 33.7%; Pred. No. 9, 3e-22;
Matches 114; Conservative 40; Mismatches 86; Indels 98; Gaps 14;

QY 109 GYAERKGEREMODAHVILNDITECRPPSLITRVSYAVFDHGGRIRASKPAQNLH 168
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 60 GY-ASSPCKRSMEDFEYTRIDVEG-----ELVGLGFVFDHGGRARAEEVYQNLF 110
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 169 QNLIRKPKGDVLSVEKTVKRCLLDTPFKHTDEFLKQASOKPAMK-DGSTATCVLAVDN 227
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 111 SNLR-HPK--FIS---DTGAIDADAVNQDSEFLKSENSQ---RDAGSTASTAILVD 161
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 228 ILVIANIGDSRALICRYNEESOKHAALSLSKEHNPQYERMRIOKAGNVR---DGRVL 284
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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DQ 162 RLVAANQDGRAVIGCN-----ALAVSRDHPQSDSRQRIEDAGGFVMAQTRVNG 215
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 285 GILVYSISIDGQYKRCGYTSVPDIR-----SEKQTYRNDOSFASAAVLGNHLYAVN 310
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 216 GVLAVSRFGRLKQF-VVAPELEIQLVFCQNLILKATLLTIENLWISIVYL 274
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 311 -----RCQLTPNDR-----FILACDGLFKVFTPEEAVNFILSCLEDEKIQ 351
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 275 NQTLQNLRLSLISLNKFOEEKVDSLEFLILASDGLMDVYVNEAV--ALAOSEEP-- 330
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 352 TREGKSADARYEAACNRLANKAVORGSDADNTVAVVIRGH 389
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 331 -----EGAKRLIMEAYORGSDADNTVCVVR 356
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 15
ID 015743 PRELIMINARY; PRT; 975 AA.
AC 015743;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Spalten.
GN SpA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA SPRAIN-AX3;
RX MEDLINE=98252837; PubMed=9585512;
RA Aubry L., Fritsch R.A.;
RT Spalten, a protein containing Galpha-protein-like and PP2C domains,
RT is essential for cell-type differentiation in Dictyostelium.";
RL Genes Dev. 12:1525-1538(1998).
DR EMBL; AF019965; AAB70844.1; -.
DR HSSP; P35813; IAG0.
DR InterPro; IPR001019; Gprotein_alpha.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00503; G-alpha; 1.
DR Pfam; PF00481; PP2C; 1.
DR Prodom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G-alpha; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C-StG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 975 AA; 109016 MW; BB8322F5026D2A4F CRC64;

Query Match 18.2%; Score 368; DB 5; Length 975;
Best Local Similarity 29.1%; Pred. No. 3, 5e-21;
Matches 118; Conservative 56; Mismatches 152; Indels 80; Gaps 17;

QY 8 PEPEKSPRAAGKEAOKGLPLDDLPASSSTDSSGGPLFLFDLPASSGDSGLATIS 67
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 620 KPPEKRPFL--KEPKKPKV--ESKPKK-----PPIPEKPEKPEKPEP 661
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 68 QWATEGCAKAKRTS-----EEKNGSEEL-----VEKKYCKASVIFGLKTYAERKE 117
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 662 KEPRKTPPEKRTKYVDGAASKKNKADSCGNGGVSKTKLSG--FG-----SLQGR 713
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 118 REEMODAHVILNDITECR---PPSSLITRVSYAVFDHGGRIRASKPAQNLH 172
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 714 RKNMEDHVLINMLNAVATYNGPPKDI--PLSYAVYDGHGRTSTLLPEPVHNCILVS 771
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 173 KRFKPGDVLSVEKTVKRCLLDTPFKHTDEFLKQASOKPAMKDGSTATCVLAVDNILYIA 232
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 772 QSFRRGQ-----YQAFRDYVABADDIVIEKE-----KSGTGVSAALLVGNKILYTA 818
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 233 NLGSRATLCRYNEESOKHAALSLSKEHNPQYERMRIOKAGNVRDGVGLV 287
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 819 NVGSEIYLARAQPNANPKNPGVTPYVPLVSTYKHLASDQKKRKYVTDLGMILFNLFGSL 878
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```


PT asthma) -
 XX
 PS Claim 1; Column 43-46; 38pp; English.
 XX
 CC The present invention relates to isolated and purified cDNA encoding a
 CC human hydrolase-like molecule (HLM), designated HLM-1 to HLM-8. The
 CC HLM DNAs and polypeptides are useful for diagnosing, treating or
 CC preventing cell proliferation disorders and autoimmune disorders. Cell
 CC proliferation disorders include cancers, autoimmune disorders include
 CC AIDS (acquired immune deficiency syndrome). The present sequence
 CC is a HLM protein of the invention.
 XX
 SO Sequence 392 AA;
 Query Match 100.0%; Score 2018; DB 22; Length 392;
 Best Local Similarity 100.0%; Pred. No. 5,7e-187;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MDLFGDLPEPERSPPRPAKGEAKGKPLFDLPPASSTDSGGGGLFDDLPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRPAKGEAKGKPLFDLPPASSTDSGGGGLFDDLPASSGDSG 60
 OY 61 SLATISOMVTEKGAKRKTSEEEKNGSEELVEKKVKASSVIFGLKGYAERKGEREE 120
 DB 61 SLATISOMVTEKGAKRKTSEEEKNGSEELVEKKVKASSVIFGLKGYAERKGEREE 120
 OY 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDGHCIRASKFAAQNHLIRKPKGDV 180
 DB 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDGHCIRASKFAAQNHLIRKPKGDV 180
 OY 181 ISVEKTVKRCLLDFPKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYLANLGDSPAI 240
 DB 181 ISVEKTVKRCLLDFPKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYLANLGDSPAI 240
 OY 241 LCARYNEESQKHAALSLSKENHPTQYEERMRIQKAGNRRDGRVLGVLEVSISIGDGQYKR 300
 DB 241 LCARYNEESQKHAALSLSKENHPTQYEERMRIQKAGNRRDGRVLGVLEVSISIGDGQYKR 300
 OY 301 CGVTSVPDIRRCQLTLPNDRFTLLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRREGSKAAD 360
 DB 301 CGVTSVPDIRRCQLTLPNDRFTLLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRREGSKAAD 360
 OY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 RESULT 2
 ABB05726
 ID ABB05726 standard; Protein; 392 AA.
 XX
 AC ABB05726;
 XX
 DT 30-APR-2002 (first entry)
 XX
 DE Human signal transduction protein clone tes3_31j30.
 XX
 KW Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200198454-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 25-APR-2001; 2001MO-IB02050.
 XX
 PR 25-APR-2000; 2000US-199380P.
 XX
 PA (GEHU) GERMAN HUMAN GENOME PROJECT.
 XX
 PI Wiemann S; *

XX
 DR WPI; 2002-055860/07.
 DR N-PSDB; ABA93763.
 XX
 PT Human cDNA sequences and clones derived from human fetal brain, fetal
 PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
 PT screening and therapy -
 XX
 PS Claim 1; Page 377; 61pp; English.
 XX
 CC The present invention describes assemblies and computer readable media
 CC comprising novel human cDNA sequences and clones derived from human
 CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 CC present invention which encode the proteins given in ABB05662 to
 CC ABB05729. The human cDNA sequences and clones can be used in gene
 CC therapy. The clones may be used in profiling assays, for providing large arrays
 CC of human genetic material for implementing large-scale screening
 CC strategies and for treating diseases via gene therapy procedures.
 XX
 SO Sequence 392 AA;
 Query Match 100.0%; Score 2018; DB 23; Length 392;
 Best Local Similarity 100.0%; Pred. No. 5,7e-187;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MDLFGDLPEPERSPPRPAKGEAKGKPLFDLPPASSTDSGGGGLFDDLPASSGDSG 60
 DB 1 MDLFGDLPEPERSPPRPAKGEAKGKPLFDLPPASSTDSGGGGLFDDLPASSGDSG 60
 OY 61 SLATISOMVTEKGAKRKTSEEEKNGSEELVEKKVKASSVIFGLKGYAERKGEREE 120
 DB 61 SLATISOMVTEKGAKRKTSEEEKNGSEELVEKKVKASSVIFGLKGYAERKGEREE 120
 OY 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDGHCIRASKFAAQNHLIRKPKGDV 180
 DB 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDGHCIRASKFAAQNHLIRKPKGDV 180
 OY 181 ISVEKTVKRCLLDFPKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYLANLGDSPAI 240
 DB 181 ISVEKTVKRCLLDFPKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYLANLGDSPAI 240
 OY 241 LCARYNEESQKHAALSLSKENHPTQYEERMRIQKAGNRRDGRVLGVLEVSISIGDGQYKR 300
 DB 241 LCARYNEESQKHAALSLSKENHPTQYEERMRIQKAGNRRDGRVLGVLEVSISIGDGQYKR 300
 OY 301 CGVTSVPDIRRCQLTLPNDRFTLLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRREGSKAAD 360
 DB 301 CGVTSVPDIRRCQLTLPNDRFTLLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRREGSKAAD 360
 OY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 RESULT 3
 ABB12317
 ID ABB12317 standard; peptide; 421 AA.
 XX
 AC ABB12317;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human protein phosphatase 2C homologue, SEQ ID NO:2687.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;

PR 25-SEP-2000: 2000US-0234998.
PR 26-SEP-2000: 2000US-0235484.
PR 27-SEP-2000: 2000US-0235834.
PR 27-SEP-2000: 2000US-0235836.
PR 29-SEP-2000: 2000US-0236327.
PR 29-SEP-2000: 2000US-0236357.
PR 29-SEP-2000: 2000US-0236358.
PR 29-SEP-2000: 2000US-0236359.
PR 29-SEP-2000: 2000US-0236370.
PR 02-OCT-2000: 2000US-0236802.
PR 02-OCT-2000: 2000US-0237037.
PR 02-OCT-2000: 2000US-0237038.
PR 02-OCT-2000: 2000US-0237039.
PR 13-OCT-2000: 2000US-0237040.
PR 13-OCT-2000: 2000US-0239935.
PR 13-OCT-2000: 2000US-0239937.
PR 20-OCT-2000: 2000US-0240960.
PR 20-OCT-2000: 2000US-0241221.
PR 20-OCT-2000: 2000US-0241785.
PR 20-OCT-2000: 2000US-0241786.
PR 20-OCT-2000: 2000US-0241787.
PR 20-OCT-2000: 2000US-0241808.
PR 20-OCT-2000: 2000US-0241809.
PR 01-NOV-2000: 2000US-0244617.
PR 08-NOV-2000: 2000US-0246474.
PR 08-NOV-2000: 2000US-0246475.
PR 08-NOV-2000: 2000US-0246476.
PR 08-NOV-2000: 2000US-0246477.
PR 08-NOV-2000: 2000US-0246478.
PR 08-NOV-2000: 2000US-0246523.
PR 08-NOV-2000: 2000US-0246524.
PR 08-NOV-2000: 2000US-0246525.
PR 08-NOV-2000: 2000US-0246526.
PR 08-NOV-2000: 2000US-0246527.
PR 08-NOV-2000: 2000US-0246528.
PR 08-NOV-2000: 2000US-0246532.
PR 08-NOV-2000: 2000US-0246539.
PR 08-NOV-2000: 2000US-0246610.
PR 08-NOV-2000: 2000US-0246611.
PR 08-NOV-2000: 2000US-0246613.
PR 17-NOV-2000: 2000US-0249207.
PR 17-NOV-2000: 2000US-0249208.
PR 17-NOV-2000: 2000US-0249209.
PR 17-NOV-2000: 2000US-0249210.
PR 17-NOV-2000: 2000US-0249211.
PR 17-NOV-2000: 2000US-0249212.
PR 17-NOV-2000: 2000US-0249213.
PR 17-NOV-2000: 2000US-0249214.
PR 17-NOV-2000: 2000US-0249215.
PR 17-NOV-2000: 2000US-0249216.
PR 17-NOV-2000: 2000US-0249217.
PR 17-NOV-2000: 2000US-0249218.
PR 17-NOV-2000: 2000US-0249219.
PR 17-NOV-2000: 2000US-0249224.
PR 17-NOV-2000: 2000US-0249225.
PR 17-NOV-2000: 2000US-0249226.
PR 17-NOV-2000: 2000US-0249227.
PR 17-NOV-2000: 2000US-0249228.
PR 17-NOV-2000: 2000US-0249229.
PR 01-DEC-2000: 2000US-0250160.
PR 01-DEC-2000: 2000US-0250391.
PR 05-DEC-2000: 2000US-0251030.
PR 05-DEC-2000: 2000US-0251988.
PR 05-DEC-2000: 2000US-0256719.
PR 06-DEC-2000: 2000US-0251479.
PR 08-DEC-2000: 2000US-0251856.
PR 08-DEC-2000: 2000US-0251868.
PR 08-DEC-2000: 2000US-0251869.
PR 08-DEC-2000: 2000US-0251899.
PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259678.

XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PT Rosen CA, Barrash SC, Ruben SM;
XX
XX WPI: 2001-465566/50.
DR N-PSDB: AAS41436.
XX
XX Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases.
XX
XX Claim 11: SEQ ID NO.1562; 1180pp; English.
XX
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AA540785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma) cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. influenza). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
CC
XX
SQ Sequence 441 AA:

Query Match 100.0%; Score 2018; DB 22; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.9e-187;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPPEPRSPAPAKGKAGKGLFDDLPASSSTDSGSGPLFDDLPASSGSG 60
DB 50 MDLFGDLPPEPRSPAPAKGKAGKGLFDDLPASSSTDSGSGPLFDDLPASSGSG 109

QY 61 SLATISQWMTTECKGAKKRTSEEEKNGSEELVEKKYCKKASVYFGKGVAMERKGERE 120
DB 110 SLATISQWMTTECKGAKKRTSEEEKNGSEELVEKKYCKKASVYFGKGVAMERKGERE 169

QY 121 MODAVIILNDITTECPRPSSLTIRVSYFVPGGCGTRASPANLHQLTRKPKGDY 180
DB 170 MODAVIILNDITTECPRPSSLTIRVSYFVPGGCGTRASPANLHQLTRKPKGDY 229

QY 181 ISVEKTVKRCLLDTFKHTDEEFLKQASSQPKMKDGSATCYLAVNDILYIANLDSRAI 240
DB 230 ISVEKTVKRCLLDTFKHTDEEFLKQASSQPKMKDGSATCYLAVNDILYIANLDSRAI 289

QY 241 ICRVNEESQKHAALSLSKEHNPTQYEEEMRIQKAGNVRGVRVLEYSRISGGOYKR 300
DB 290 ICRVNEESQKHAALSLSKEHNPTQYEEEMRIQKAGNVRGVRVLEYSRISGGOYKR 349

QY 301 CGVTSVPDIRRCQLTPMDREFILACDGLFKYFTEPEAVNFILSCLEDEKIQTRKGSAD 360
DB 350 CGVTSVPDIRRCQLTPMDREFILACDGLFKYFTEPEAVNFILSCLEDEKIQTRKGSAD 409

QY 361 ARYEACNRLANKAVGSGSADNTVWVVRIGH 392
DB 410 ARYEACNRLANKAVGSGSADNTVWVVRIGH 441

RESULT 6
AAU22933
ID AAU22933 standard; Protein: 446 AA.

XX	AAU22933;		PR	12-SEP-2000;	2000US-0231968.
AC			PR	14-SEP-2000;	2000US-0232397.
XX	17-DEC-2001 (first entry)		PR	14-SEP-2000;	2000US-0232398.
DT			PR	14-SEP-2000;	2000US-0232399.
XX			PR	14-SEP-2000;	2000US-0232400.
DE	Novel human enzyme polypeptide #19.		PR	14-SEP-2000;	2000US-0232401.
XX			PR	14-SEP-2000;	2000US-0233063.
KW	Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;		PR	14-SEP-2000;	2000US-0233064.
KW	lyase; hyperproliferative disorder; immunodeficiency disorder;		PR	21-SEP-2000;	2000US-0234023.
KW	autoimmune disorder; neurological disorder; metabolic disorder;		PR	25-SEP-2000;	2000US-0234927.
KW	inflammatory disorder; cardiovascular disorder; reproductive disorder;		PR	25-SEP-2000;	2000US-0234929.
KW	blood-related disorder; infectious disorder; cytostatic; anti arthritic;		PR	25-SEP-2000;	2000US-0234998.
KW	nephrotropic; anticoagulant.		PR	26-SEP-2000;	2000US-0235484.
XX			PR	27-SEP-2000;	2000US-0235834.
OS	Homo sapiens.		PR	27-SEP-2000;	2000US-0235836.
XX			PR	29-SEP-2000;	2000US-0236327.
PN	WO200155301-A2.		PR	29-SEP-2000;	2000US-0236367.
XX			PR	29-SEP-2000;	2000US-0236368.
PD	02-AUG-2001.		PR	29-SEP-2000;	2000US-0236369.
XX			PR	29-SEP-2000;	2000US-0236370.
XX	17-JAN-2001; 2001WO-US01239.		PR	02-OCT-2000;	2000US-0236802.
PF			PR	02-OCT-2000;	2000US-0237037.
XX			PR	02-OCT-2000;	2000US-0237039.
PR	31-JAN-2000; 2000US-0179065.		PR	02-OCT-2000;	2000US-0237040.
PR	04-FEB-2000; 2000US-0180628.		PR	13-OCT-2000;	2000US-0239935.
PR	24-FEB-2000; 2000US-0184664.		PR	20-OCT-2000;	2000US-0240960.
PR	02-MAR-2000; 2000US-0186350.		PR	20-OCT-2000;	2000US-0241221.
PR	16-MAR-2000; 2000US-0189874.		PR	20-OCT-2000;	2000US-0241785.
PR	17-MAR-2000; 2000US-0190076.		PR	20-OCT-2000;	2000US-0241786.
PR	18-APR-2000; 2000US-0198123.		PR	20-OCT-2000;	2000US-0241787.
PR	19-MAY-2000; 2000US-0205515.		PR	20-OCT-2000;	2000US-0241808.
PR	07-JUN-2000; 2000US-0209467.		PR	20-OCT-2000;	2000US-0241809.
PR	28-JUN-2000; 2000US-0214886.		PR	20-OCT-2000;	2000US-0241826.
PR	30-JUN-2000; 2000US-0215135.		PR	01-NOV-2000;	2000US-0244617.
PR	07-JUL-2000; 2000US-0216647.		PR	08-NOV-2000;	2000US-0246475.
PR	07-JUL-2000; 2000US-0216880.		PR	08-NOV-2000;	2000US-0246476.
PR	11-JUL-2000; 2000US-0217487.		PR	08-NOV-2000;	2000US-0246477.
PR	11-JUL-2000; 2000US-0217496.		PR	08-NOV-2000;	2000US-0246478.
PR	14-JUL-2000; 2000US-0218290.		PR	08-NOV-2000;	2000US-0246523.
PR	26-JUL-2000; 2000US-0220963.		PR	08-NOV-2000;	2000US-0246524.
PR	26-JUL-2000; 2000US-0220964.		PR	08-NOV-2000;	2000US-0246525.
PR	14-AUG-2000; 2000US-0224518.		PR	08-NOV-2000;	2000US-0246526.
PR	14-AUG-2000; 2000US-0224519.		PR	08-NOV-2000;	2000US-0246527.
PR	14-AUG-2000; 2000US-0225213.		PR	08-NOV-2000;	2000US-0246528.
PR	14-AUG-2000; 2000US-0225214.		PR	08-NOV-2000;	2000US-0246532.
PR	14-AUG-2000; 2000US-0225266.		PR	08-NOV-2000;	2000US-0246533.
PR	14-AUG-2000; 2000US-0225267.		PR	08-NOV-2000;	2000US-0246609.
PR	14-AUG-2000; 2000US-0225268.		PR	08-NOV-2000;	2000US-0246610.
PR	14-AUG-2000; 2000US-0225270.		PR	08-NOV-2000;	2000US-0246611.
PR	14-AUG-2000; 2000US-0225447.		PR	08-NOV-2000;	2000US-0246613.
PR	14-AUG-2000; 2000US-0225757.		PR	08-NOV-2000;	2000US-0249207.
PR	14-AUG-2000; 2000US-0225758.		PR	08-NOV-2000;	2000US-0249208.
PR	14-AUG-2000; 2000US-0225759.		PR	08-NOV-2000;	2000US-0249209.
PR	18-AUG-2000; 2000US-0226279.		PR	17-NOV-2000;	2000US-0249210.
PR	22-AUG-2000; 2000US-0226681.		PR	17-NOV-2000;	2000US-0249211.
PR	22-AUG-2000; 2000US-0226868.		PR	17-NOV-2000;	2000US-0249212.
PR	22-AUG-2000; 2000US-0227182.		PR	17-NOV-2000;	2000US-0249213.
PR	23-AUG-2000; 2000US-0227009.		PR	17-NOV-2000;	2000US-0249214.
PR	30-AUG-2000; 2000US-0228924.		PR	17-NOV-2000;	2000US-0249215.
PR	01-SEP-2000; 2000US-0229287.		PR	17-NOV-2000;	2000US-0249216.
PR	01-SEP-2000; 2000US-0229343.		PR	17-NOV-2000;	2000US-0249217.
PR	01-SEP-2000; 2000US-0229344.		PR	17-NOV-2000;	2000US-0249218.
PR	01-SEP-2000; 2000US-0229345.		PR	17-NOV-2000;	2000US-0249219.
PR	05-SEP-2000; 2000US-0229509.		PR	17-NOV-2000;	2000US-0249220.
PR	05-SEP-2000; 2000US-0229513.		PR	17-NOV-2000;	2000US-0249221.
PR	06-SEP-2000; 2000US-0230437.		PR	17-NOV-2000;	2000US-0249222.
PR	06-SEP-2000; 2000US-0230438.		PR	17-NOV-2000;	2000US-0249223.
PR	08-SEP-2000; 2000US-0231242.		PR	17-NOV-2000;	2000US-0249244.
PR	08-SEP-2000; 2000US-0231243.		PR	17-NOV-2000;	2000US-0249245.
PR	08-SEP-2000; 2000US-0231244.		PR	17-NOV-2000;	2000US-0249246.
PR	08-SEP-2000; 2000US-0231413.		PR	17-NOV-2000;	2000US-0249255.
PR	08-SEP-2000; 2000US-0231414.		PR	17-NOV-2000;	2000US-0249257.
PR	08-SEP-2000; 2000US-0232080.		PR	17-NOV-2000;	2000US-0249299.
PR	08-SEP-2000; 2000US-0233081.		PR	17-NOV-2000;	2000US-0249300.
PR			PR	01-DEC-2000;	2000US-0250160.

```
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251968.
PR 05-DEC-2000; 2000US-0251968.
PR 06-DEC-2000; 2000US-0251479.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM.
XX
XX WPI: 2001-465566/50.
XX
XX N-PSDB: AAS40803.
XX
XX Novel polypeptides and polynucleotides useful for diagnosing,
XX preventing, treating neural, immune system, muscular, reproductive,
XX pulmonary, cardiovascular, renal, proliferative disorders and cancerous
XX diseases.
XX
XX Claim 11: SEQ ID NO 929; 1180bp; English.
XX
XX
XX The present invention relates to the isolation of novel human enzyme
XX polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
XX encoding them. The enzyme polypeptides of the invention may comprise the
XX functional classes of oxidoreductases, transferases, hydrolases, lyases,
XX isomerases or ligases. The sequences of the invention are useful in the
XX diagnosis, treatment, prevention and/or prognosis of a wide range of
XX disorders, including hyperproliferative disorders (e.g. cancer),
XX immunodeficiency disorders (e.g. AIDS) autoimmune disorders
XX (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
XX metabolic disorders (e.g. phenylketonuria), inflammatory disorders
XX (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
XX blood-related disorders (e.g. haemophilia), reproductive disorders
XX (e.g. infertility) and infectious disorders (e.g. influenza). The
XX polynucleotides of the invention can also be used in gene therapy.
XX AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
XX invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIFO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 446 AA:
XX
XX Query Match 100.0%; Score 2018; DB 22; Length 446;
XX Best Local Similarity 100.0%; Pred. No. 7e-187;
XX Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MDLFGDLPEPERSPPAAGKAKQKGLLEFDDLPASSTDSGSGGPLEFDDLPASSGDSG 60
XX 55 MDLFGDLPEPERSPPAAGKAKQKGLLEFDDLPASSTDSGSGGPLEFDDLPASSGDSG 114
XX
XX 61 STATISOMVKTGKAGAKRTSEBKNKSGSELEVKVCASSVIFGLKGYAEKRCREE 120
XX 115 STATISOMVKTGKAGAKRTSEBKNKSGSELEVKVCASSVIFGLKGYAEKRCREE 174
XX
XX 121 MODAHVILNDITEECRPPSSILITRVSFAVFDGSGIRSKAFAONLHONLIRKFPFGDV 180
XX 175 MODAHVILNDITEECRPPSSILITRVSFAVFDGSGIRSKAFAONLHONLIRKFPFGDV 234
XX
XX 181 ISEKTVKRCCLDTPFKHDEEFLKQASSOKPAWKDSTATCYLVANDNITYANLGSRAI 240
XX 235 ISEKTVKRCCLDTPFKHDEEFLKQASSOKPAWKDSTATCYLVANDNITYANLGSRAI 294
XX
XX 241 LCRVNEESOKHAALSLSEKHNPTOYEEBMTIOKAGNVNDGVLGVLEVSNSIGDGYKR 300
XX 295 LCRVNEESOKHAALSLSEKHNPTOYEEBMTIOKAGNVNDGVLGVLEVSNSIGDGYKR 354
XX
XX
XX 301 CGVTSVPDIRRCQFTPNDRFILLACDGLFKVFPPEEAVNFILSLCEDEKIQTRKSKAAD 360
XX 355 CGVTSVPDIRRCQFTPNDRFILLACDGLFKVFPPEEAVNFILSLCEDEKIQTRKSKAAD 414
XX
XX 361 ARVEACNRLANKRAVORGSAADNVTVVVRIGH 392
XX 415 ARVEACNRLANKRAVORGSAADNVTVVVRIGH 446
XX
XX
XX RESULT 7
XX AAB92585
XX ID AAB92585 standard; protein: 392 AA.
XX
XX AC AAB92585;
XX
XX DT 26-JUN-2001 (first entry)
XX
XX DE Human protein sequence SEQ ID NO:10816.
XX
XX KW Human: primer: detection: diagnosis: antisense therapy: gene therapy.
XX OS Homo sapiens.
XX
XX PN EP1074617-A2.
XX
XX PD 07-FEB-2001.
XX
XX PF 28-JUL-2000; 2000EP-0116126.
XX
XX PR 29-JUL-1999; 99JP-0248036.
XX PR 27-AUG-1999; 99JP-0300253.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.
XX
XX PA (HELI-) HELIX RES INSR.
XX
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI: 2001-318749/34.
XX
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX
XX PS Claim 8: SEQ ID 10816; 2537bp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03156 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences. AAB92446 to
XX AAB95883 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
XX
XX Sequence 392 AA:
```

Query Match 99.9%; Score 2015; DB 22; Length 392;
Best Local Similarity 99.7%; Pred. No. 1.1e-186;
Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFDLPEPPSPRPAAGKEAKGKPLFDLPPASSTDSGSGPLFDLPPASSGDSG 60
D 1 MDLFDLPEPPSPRPAAGKEAKGKPLFDLPPASSTDSGSGPLFDLPPASSGDSG 60
QY 61 SLATSIQMVKTEGKARKTSEEEKNGSEELVEKKVCKASVIFGLGYAERKGEREE 120
D 61 SLATSIQMVKTEGKARKTSEEEKNGSEELVEKKVCKASVIFGLGYAERKGEREE 120
QY 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHCIGIRASKEFAQNLHONLIRKPKGDV 180
D 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHCIGIRASKEFAQNLHONLIRKPKGDV 180
QY 181 ISVEKTVKRLDLPFKHDEEFLKQASSQKPAKMGSTATCVLAVDNILYANLGDSPAI 240
D 181 ISVEKTVKRLDLPFKHDEEFLKQASSQKPAKMGSTATCVLAVDNILYANLGDSPAI 240
QY 241 LCRVNEESQKHAALSLSKENHPTQYEERMRIQKAGNVRDGRVLGYLEVSRISIDGQYKR 300
D 241 LCRVNEESQKHAALSLSKENHPTQYEERMRIQKAGNVRDGRVLGYLEVSRISIDGQYKR 300
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEAVNFIILSCLEDEKIQTRGKSAAD 360
D 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEAVNFIILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVORGADNVTVMVVRIGH 392
D 361 ARYEACNRLANKAVORGADNVTVMVVRIGH 392

RESULT 8
AAM38769
ID AAM38769 standard; Protein: 392 AA.

AC AAM38769;
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 1914.

XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW Peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW Amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW Chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.

XX Homo sapiens.
OS
PN MO20015312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000MO-US34263.

XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang XT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang Z, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.
DR N-PSDB; AA157925.

PT Novel nucleic acids and polypeptides, useful for treating disorders
PS such as central nervous system injuries -
XX Example 3; SEQ ID NO 1914; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161365) and
CC the encoded polypeptides (AAM38642-AAM42213) with noctropic.
CC Immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 392 AA;

Query Match 99.8%; Score 2014; DB 22; Length 392;
Best Local Similarity 99.7%; Pred. No. 1.4e-186;
Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFDLPEPPSPRPAAGKEAKGKPLFDLPPASSTDSGSGPLFDLPPASSGDSG 60
D 1 MDLFDLPEPPSPRPAAGKEAKGKPLFDLPPASSTDSGSGPLFDLPPASSGDSG 60
QY 61 SLATSIQMVKTEGKARKTSEEEKNGSEELVEKKVCKASVIFGLGYAERKGEREE 120
D 61 SLATSIQMVKTEGKARKTSEEEKNGSEELVEKKVCKASVIFGLGYAERKGEREE 120
QY 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHCIGIRASKEFAQNLHONLIRKPKGDV 180
D 121 MODAHVILNDITEECRPPSSILTRVSYFAVFDGHCIGIRASKEFAQNLHONLIRKPKGDV 180
QY 181 ISVEKTVKRLDLPFKHDEEFLKQASSQKPAKMGSTATCVLAVDNILYANLGDSPAI 240
D 181 ISVEKTVKRLDLPFKHDEEFLKQASSQKPAKMGSTATCVLAVDNILYANLGDSPAI 240
QY 241 LCRVNEESQKHAALSLSKENHPTQYEERMRIQKAGNVRDGRVLGYLEVSRISIDGQYKR 300
D 241 LCRVNEESQKHAALSLSKENHPTQYEERMRIQKAGNVRDGRVLGYLEVSRISIDGQYKR 300
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEAVNFIILSCLEDEKIQTRGKSAAD 360
D 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEAVNFIILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVORGADNVTVMVVRIGH 392
D 361 ARYEACNRLANKAVORGADNVTVMVVRIGH 392

RESULT 9
ABG09937
ID ABG09937 standard; Protein: 378 AA.

XX ABG09937;
XX
XX
XX

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #9928.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 138 AA:

Query Match 22.2%; Score 447.5; DB 22; Length 138;
Best Local Similarity 87.4%; Pred. No. 3,1e-35;
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DB 10 RGRVYGVLEVSRISIDGGYKKCVTSVPDIRRCQLTPNDRFILLACDGLFKVETPEEAY 69
OY 339 NFIISGLEDEKIQTRGKSAADARVEAACNRLANK-AVORGSA 380
DB 70 NFIISGLEDEKIQTRGKSAADARVEALQHAQQGKSGRGA 112

RESULT 13
AAG18068
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XX
AC AAG18068;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19329.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 01-JUL-1999; 99US-0141842.
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PR 02-JUL-1999; 99US-0142055.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 07-SEP-1999; 99US-0151930.
PR 10-SEP-1999; 99US-0152353.
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 13-OCT-1999; 99US-0159283.
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DB 84 LPDASLDF--PGTL--RCAHFAIYDGHGRLAAEFARKHLHLNVLVSAGPRELIDV--KVA 138
QY 188 KRCLIDTFKHTDEEFLKQASOKPAWKDGSATCVLANVDNLIYIANLGSBRAILCR---- 243
DB 139 KKALIEGFRKRTDELLQKSVS--GGMODGATAVACWILDOKFVANIGDAKAVLARSSSTT 196
QY 244 -----VNEESQKHAALSLSKENHPTQYERRRIQKAGNV--RDGRVIGVLEYSRISIGDQ 297
DB 197 NELGNHTEAGNPILKAIYLTREHKAITYPQERSRIQKSGGVISNGRLQGRTEVSRFAFGDRH 256
QY 299 YKRCGVTSVPDIRRCQUTPNDRFILLACDGLFKV 331
DB 257 FRKCGVATPDIAHAFELTERENFMILGCDGLMEV 290

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XX
DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 19328.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0121800.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.

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PR 21-OCT-1999; 99US-0160815.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 21.4%; Score 431.5; DB 21; Length 305;
Best Local Similarity 37.2%; Pred. No. 3,6e-33;
Matches 102; Conservative 59; Mismatches 86; Indels 27; Gaps 8;

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DB 34 KAKSEEVSGGEAVANAGNKRRAEDKPSFVSEKKEFLVEADVEDKGAHRTMEDVWV 93
OY 128 LNDITECRPPSSLITRVSYFAVFDHGIGIRASKFAAQNHLQNLIRKPKGDVISEKTV 187
DB 94 LPDKSLDF--PGTL--RCNAFAIYDGHGIRLAELFAKKHLHLNVISAGLPRLLDY--KVA 148
OY 188 KRCLLDTEFKHTDEEFLKQASSQKPAKMDGSTATCVLAVDNIYIANTLGDRAILCR---- 243
DB 149 KKAILEGFRKTDLLQKSVS--GGMDGATAVCWILDOKVFVANIGDAKAVLARSTT 206
OY 244 -----YNEESQKHAALSLSKEHNPTQYERMRIOKAGNV--RDGRVLGVLEVSRSIDGQ 297
DB 207 NELGNHTEAGNPLKAIIVLIRHKAITYPERERIOKSGVYSSNGRLQGRLEVSRAFGDRH 266
OY 298 YKRCGVTSVPDIRCOLFPNDRIILLACDGLFKY 331
DB 267 FKKFGVSATPDIAHAFELTERENFMILGDDGIMEV 300

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AC AAG03424;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 7505.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PE 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Mline Edwards J, Duclert A, Giordano J;
XX
DR WPI: 2000-500381/45.
XX
DR N-PSDB: AAC03430.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX
PS Claim 13; SEQ ID 7505; 71pp + CD-ROM; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC regulatory sequences and to design expression and secretion vectors.
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SQ Sequence 86 AA;

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DB 1 MODAVIINDITECRPPSSLITRVSYFAVFDHGIGIRASKFAAQNHLQNLIRKPKGDV 60
OY 181 ISEKTVKRCLLDTEFKHTDEEFLKQ 205
DB 61 ISEKTVKRCLLDTEFKHTDEEFLKQ 85

Search completed: January 17, 2003, 17:45:41
Job time : 41 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:44:19 ; Search time 12 Seconds
(without alignments)
649,365 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 1 MDLFGDLPEPRSPRPAAGK.....KAVQSGADNTVMVVRIGH 392

Sequence: 1 MDLFGDLPEPRSPRPAAGK.....KAVQSGADNTVMVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	395.5	19.6	274	10	US-09-860-351-4
3	370.5	18.4	353	10	US-09-828-302-14
4	338	16.7	382	10	US-09-972-741-2
5	319	15.8	390	9	US-10-072-130-3
6	317.5	15.7	281	10	US-09-801-368-278
7	314	15.6	372	9	US-09-973-941-4
8	314	15.6	372	10	US-09-973-963-4
9	314	15.6	372	10	US-09-973-064-4
10	314	15.6	372	10	US-09-973-077-4
11	314	15.6	372	10	US-09-973-063-4
12	314	15.6	372	10	US-09-973-964-4
13	314	15.6	372	10	US-09-975-072-4
14	314	15.6	372	10	US-09-972-038-4
15	314	15.6	372	10	US-09-972-357-4
16	314	15.6	372	10	US-09-973-965-4
17	313	15.5	478	9	US-10-072-130-1
18	313	15.5	478	9	US-10-072-130-4
19	312	15.5	400	10	US-09-925-300-1254

20	309	15.3	373	10	US-09-925-300-1655	Sequence 1655, App
21	294	14.6	387	10	US-09-866-987-9	Sequence 9, App1
22	283	14.0	352	10	US-09-860-351-2	Sequence 2, App1
23	273	13.5	371	10	US-09-828-302-15	Sequence 15, App1
24	258.5	12.8	491	9	US-10-114-893-69	Sequence 69, App1
25	240.5	11.9	428	10	US-09-900-715-2	Sequence 2, App1
26	200.5	9.9	459	10	US-09-866-987-8	Sequence 8, App1
27	191	9.5	149	10	US-09-860-351-6	Sequence 6, App1
28	185.5	9.2	2026	10	US-09-801-368-86	Sequence 86, App1
29	178	8.8	504	9	US-10-158-895-2	Sequence 2, App1
30	178	8.8	504	12	US-10-123-427-2	Sequence 2, App1
31	178	8.8	313	9	US-10-158-895-43	Sequence 43, App1
32	178	8.8	313	9	US-10-158-895-11	Sequence 11, App1
33	176	8.7	504	12	US-10-123-427-6	Sequence 6, App1
34	154	7.6	114	10	US-09-860-351-5	Sequence 5, App1
35	153.5	7.6	282	10	US-09-752-820A-2	Sequence 2, App1
36	153.5	7.6	282	10	US-09-813-319A-2	Sequence 2, App1
37	128.5	6.4	143	10	US-09-866-987-10	Sequence 10, App1
38	114	5.6	293	9	US-09-902-523-42	Sequence 42, App1
39	111	5.5	514	9	US-09-866-987-12	Sequence 12, App1
40	103	5.1	145	10	US-09-752-820A-6	Sequence 6, App1
41	103	5.1	145	10	US-09-813-319A-6	Sequence 6, App1
42	103	5.1	146	10	US-09-752-820A-4	Sequence 4, App1
43	103	5.1	146	9	US-09-813-319A-4	Sequence 4, App1
44	103	5.1	475	9	US-09-854-133-193	Sequence 193, App
45	103	5.1	475	10	US-09-738-973-193	Sequence 193, App

ALIGNMENTS

RESULT 1
US-09-935-124A-2
Sequence 2, Application US/09935124A
Patent No. US2002013603A1
GENERAL INFORMATION:
APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Hogenberger, Jakob
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210us
CURRENT APPLICATION NUMBER: US/09/935, 124A
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284,760
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-124A-2

Query Match 100.0%; Score 2018; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.8e-172;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPRSPRPAAGKEAKGKGLFDLPASSSDSGGGLFDLPASSGDSG 60
DB 1 MDLFGDLPEPRSPRPAAGKEAKGKGLFDLPASSSDSGGGLFDLPASSGDSG 60
QY 61 STATSIQWVTEKRGKAKRTSEKNSGESELYEKKYKASVYFGIKGVNERGEREE 120
DB 61 STATSIQWVTEKRGKAKRTSEKNSGESELYEKKYKASVYFGIKGVNERGEREE 120
QY 121 MODAHVILNDITECRPPSSILTRVSYFAVEFGGCTGASFAAONHONLIRKPKD 180
DB 121 MODAHVILNDITECRPPSSILTRVSYFAVEFGGCTGASFAAONHONLIRKPKD 180
QY 181 ISVEKTVKRCILDFPKHTDEFLKQASOKPAWKGSATATCYAVNDIILYINLID 240
DB 181 ISVEKTVKRCILDFPKHTDEFLKQASOKPAWKGSATATCYAVNDIILYINLID 240

QY	241	LCRTNEESQKIAAALSLSKSEHPQTYEEMRMQRKGAVRQGRVLTGLVEVRSRSTGDDGYKR	300
Db	241	LCRTNEESQKIAAALSLSKSEHPQTYEEMRMQRKGAVRQGRVLTGLVEVRSRSTGDDGYKR	300
QY	301	CGVTSVPDIRRCQLTLPNDRFLLTLCDCGLFKFKEPPEEAVNFISSLCEDEKIQTRRGKSAAD	360
Db	301	CGVTSVPDIRRCQLTLPNDRFLLTLCDCGLFKFKEPPEEAVNFISSLCEDEKIQTRRGKSAAD	360
QY	361	ARYEACNRLLANKAVQRGSADNTVMVVRIGH	392
Db	361	ARYEACNRLLANKAVQRGSADNTVMVVRIGH	392

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RESULT 2
US-09-860-351-4
: Sequence 4, Application US/09860351
: Patent No. US20020077463A1
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: APPLICANT: Meyers, Rachel
: TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
: TITLE OF INVENTION: AND USES THEREFOR
: FILE REFERENCE: 38155-20013-00
: CURRENT APPLICATION NUMBER: US/09/860,351
: CURRENT FILING DATE: 2001-05-17
: PRIORITY FILING DATE: 2000-05-19
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 274
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Consensus amino acid
: US-09-860-351-4

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	Query Match	19.6%	Score 395.5	DB 10;	Length 274;	
	Best Local Similarity	36.7%	Pred. No. 8.4e-28;			
	Matches 106; Conservative	49;	Mismatches 79;	Indels 55;	Gaps 13;	
QY	118 REEMODAHVILINDITEECRPPSSLLTRVSFAVPFGDHGRKSRFPAONLHONI----	RK 174	:	:	:	:
Db	1 RKSMDAHIALKNLNLSSSSGKDSW----	SFAVFPGHGGSQAOKAYAGHAKHTIIAEKRS 56	:	:	:	:
QY	175 FPKGD-----VISYEKYRKCLDFTFKHTDEEFLKOASS-----	QKPAMKDGSATATCVL 223	:	:	:	:
Db	57 FPGEQPMWKMLSDLEDALESFLEA--DTDEELBRASAASANKVLTKEDLSGSGTAAVVAL 114		:	:	:	:
QY	224 AVDNILTYANTLGDSFAILICRYNESOKIAHALSLSEKHNPOTYEERMRIQKAG--	NVRD 280	:	:	:	:
Db	115 IRGNKLTVANNGDSRAVLCR--NGNAIKW-AVTLTEDHKPSNEDEERITIEAGFPYSRVSN 172		:	:	:	:
QY	281 GRVLGVLEVNSISIGGYQR-----RCG-----	VTSVDI--RCOLTPN- 317	:	:	:	:
Db	173 GRVNVGLVASRAFPGFPELKPGSKLPBESLEANYVEYIKSPEOGLVAEPDVNSTDLTPDK 232		:	:	:	:
QY	318 DRFILACDGFLKFVTPPEAVNFILSCLEDEXIQREKKSADARVEAA 366		:	:	:	:
Db	233 DEFLTLACDGLNDVVSDDQEVNDIVINSELST-----GNKSLEDPEMEA 274		:	:	:	:

RESULT 3
 US-09-028-302-14
 : Sequence 14, Application US/09828302
 : Patent No. US20020152502A1
 : GENERAL INFORMATION:
 : APPLICANT: COSTA E SILVA, OSWALDO DA
 : APPLICANT: VAN THIELEN, NOCHA
 : APPLICANT: CHEN, ROUYING
 : APPLICANT: ISHITANI, MANABU
 : TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE

```

: TITLE OF INVENTION: IN PLANTS
: FILE REFERENCE: 16313-0039
: CURRENT APPLICATION NUMBER: US/09/828,302
: CURRENT FILING DATE: 2001-08-20
: PRIOR APPLICATION NUMBER: 60/196,001
: PRIOR FILING DATE: 2000-04-07
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 14
: LENGTH: 353
: TYPE: PRN
: ORGANISM: Physcomitrella patens
US-09-828-302-14

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[illegible]

Qy 376 -----QKGSADNVTVMVVR 389
|: |:|:::|:
Db 322 SPYTRQEGCDNMSLIIVQ 340

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RESULT 4
US-09-972-741-2
: Sequence 2, Application US/09972741
: Patent No. US20020100070A1
: GENERAL INFORMATION:
: APPLICANT: Allen, Keith D.
: TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
: TITLE OF INVENTION: MAGNESIUM-DEPENDENT PROTEIN PHOSPHATASE GENE DISRUPTIONS
: FILE REFERENCE: R-723-C1P
: CURRENT APPLICATION NUMBER: US/09/972,741
: PRIORITY FILING DATE: 2001-10-08
: PRIORITY APPLICATION NUMBER: US 09/815,935
: PRIORITY FILING DATE: 2001-03-22
: PRIORITY APPLICATION NUMBER: US 60/191,235
: PRIORITY FILING DATE: 2000-03-22
: PRIORITY APPLICATION NUMBER: US 60/216,249
: PRIORITY FILING DATE: 2000-07-06
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 382
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-972-741-2
Query Match 16.7%; Score 338; DB 10; Length 382;

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Db 73 LHTIEQNIL-----ADETRDVRLVNDSELAIDEI-----NTKLVNSGCTAAVC 119
QY 222 VL---AVDNI-----LYIANLGDSRAILCRYNEESOKHAALSLSEKHNPQY 265
Db 120 VLRLWELPQSVSDSDMLAQHQKRLTYANVGDRIYLFNRGN-----SIRLTYDHKASDT 173
QY 266 EERNATQKAGCVNRGRVGLVLEVSRSIGDGOYKRGCYTSVPDIRCOLTPNDRIFILLAC 325
Db 174 LEMQREVOAGGLIMKRSRYNGMLATYRSLGDKFDSLTVVGS--PFTTSVETTSDEKFLILAC 232
QY 326 DGLFVFPPEAVNFILSCLEDEKIQOTREKGSAAADARYEACNRLANKAVOGSADNVTY 385
Db 223 DGLMVYIDDQACELIKITPEPNE-----AAKVLVRYALENGTIDNVTY 276
QY 386 MVV 388
Db 277 MVV 279

RESULT 7
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US20020164655A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,941
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-941-4

Query Match 15.6%; Score 314; DB 9; Length 372;
Best Local Similarity 27.5%; Pred. No. 2.5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY 27 LLFDD---LPPASSTDS-----GSGGPLLFDD-----LPPASSGDSG 60
Db 27 LLQDDRVTPTCHSSTSEPCSRFPDSSGSPATWDNFGIMDNRIDEPILLPPI----- 81
QY 61 SLATSIQMVTEGKGARKTSEEKNGSEELVEKKVCASSVIFGLGYAERGEREE 120
Db 82 -----KYG-----KPIKISLENGCASQIGKR--EMED 109
QY 121 MODAHVILNITEECRPSSLITRVSYFAVFDHGIGIRASKFAONLQNLIRKPKGDV 180
Db 110 RFD-----FAOLTDE-----VLRYAVYDGHGPPAADFCCHHMEKCIDMLPK--- 152
QY 181 ISVEKTVARKLLDPFKHNDDEFLKQA--SSQKPAKDGSTATCVLANVNI--LYIANLGDS 237
Db 153 ---EKNLETLTLAFLLEIDKAFSSHARLSADATLLTSGTATVALLRDGIELVVASGDS 209
QY 238 RAILCRYNEESOKHAALSLSEKHNPQYEEERMRIQKAG-----NVRGRVGLVLEVSRS 292
Db 210 RAILCR-----KGRPKMLTIDHTPERKDEKERIKKCGFYAAMNSLGGPHVNGRLAMTRS 263
QY 293 IGDGOYKRGCYTSVPDIRCOL--TPNDRIFILLACDGLFKVFPPEAVNFILSCLEDEKIQ 351
Db 264 IGDIDLKTSGVIAEPETKRIRKLHHAADSFVLVTTDGINFMVNSQETICDFVQCHDPNE-- 321
QY 352 TREKGSAAADARYEACNRLANKAVOGSADNVTYVAVRIG 391

Db 322 -----AAHAVTEQAIQYGTEDNSTAVVDFG 347
RESULT 8
US-09-973-963-4
; Sequence 4, Application US/09973963
; Patent No. US20020106676A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,963
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-963-4

Query Match 15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2.5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY 27 LLFDD---LPPASSTDS-----GSGGPLLFDD-----LPPASSGDSG 60
Db 27 LLQDDRVTPTCHSSTSEPCSRFPDSSGSPATWDNFGIMDNRIDEPILLPPI----- 81
QY 61 SLATSIQMVTEGKGARKTSEEKNGSEELVEKKVCASSVIFGLGYAERGEREE 120
Db 82 -----KYG-----KPIKISLENGCASQIGKR--EMED 109
QY 121 MODAHVILNITEECRPSSLITRVSYFAVFDHGIGIRASKFAONLQNLIRKPKGDV 180
Db 110 RFD-----FAOLTDE-----VLRYAVYDGHGPPAADFCCHHMEKCIDMLPK--- 152
QY 181 ISVEKTVARKLLDPFKHNDDEFLKQA--SSQKPAKDGSTATCVLANVNI--LYIANLGDS 237
Db 153 ---EKNLETLTLAFLLEIDKAFSSHARLSADATLLTSGTATVALLRDGIELVVASGDS 209
QY 238 RAILCRYNEESOKHAALSLSEKHNPQYEEERMRIQKAG-----NVRGRVGLVLEVSRS 292
Db 210 RAILCR-----KGRPKMLTIDHTPERKDEKERIKKCGFYAAMNSLGGPHVNGRLAMTRS 263
QY 293 IGDGOYKRGCYTSVPDIRCOL--TPNDRIFILLACDGLFKVFPPEAVNFILSCLEDEKIQ 351
Db 264 IGDIDLKTSGVIAEPETKRIRKLHHAADSFVLVTTDGINFMVNSQETICDFVQCHDPNE-- 321
QY 352 TREKGSAAADARYEACNRLANKAVOGSADNVTYVAVRIG 391
Db 322 -----AAHAVTEQAIQYGTEDNSTAVVDFG 347

RESULT 9
US-09-973-064-4
; Sequence 4, Application US/09973064
; Patent No. US20020106773A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND


```

: CURRENT APPLICATION NUMBER: US/09/973,064
: CURRENT FILING DATE: 2001-10-10
: PRIOR APPLICATION NUMBER: US 60/240,790
: PRIOR FILING DATE: 2000-10-17
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 4
: LENGTH: 372
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-973-064-4

Query Match          15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2,5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

OY 27 LFFD---LPPASSTDS-----GSGGRLFPD-----LPPASGDSG 60
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Db 27 LLODDRVTPTCHSTSEPCRSRFPDGSSPATMDNCGIMDNRIDEPILLPSI----- 81
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OY 61 SLATSIQWVTEGKARKRTSEEEKNGSELEVEKKVCASSVIFGLKGYAERKGEREE 120
|||
Db 82 -----KYG-----KPIKISLENVGASQIGKRK-ENED 109
|||
OY 121 MODAHVILNDITECRPPSSLITRVSYFAVFGHGIGIRASKFAAONLHONLIRKPKGV 180
|||
Db 110 RFD---FAQLTDE-----VLTFVAYDGHGPPAADCHTHMEKCIIMDLPR--- 152
|||
OY 181 ISEKTVKRCLLDTEFKHTDEEFLKQA--SSQKPAWKDGSATATCYLAVDNT-LYIANLGS 237
|||
Db 153 ---EKNLETLTLAFLLEIDKAFSSHARLSADATLLTSGTTATVALRDIELVAVASGDS 209
|||
OY 238 RALICRYNEESOKHAALSLSEKHNPYOYERMRIOKAG-----NVRDGYLVLEVSR 292
|||
Db 210 RALICR-----KGKPMKLTIDHTPERDEKERIKKGGFVAMNSLGGPHNGHLAMTRS 263
|||
OY 293 IGDQYKRCGVTSVPDIRCOL-TPNDRFILLACDGLFKFVTPPEAVNFILSCLEDEKIQ 351
|||
Db 264 IGDIDKTSQVIAEPETRIKRIKHNADSFVLVLTDDGINFMVNSOEICDFVNOCHDPNE-- 321
|||
OY 352 TREKSAADARYEAACNRLANKAVORGSAADVAVVVRIG 391
|||
Db 322 -----AAHAYTEQAIOYGTEDNSTAVVVRIG 347
|||

RESULT 10
US-09-973-077-4
: Sequence 4, Application US/09973077
: Patent No. US20020114799A1
: GENERAL INFORMATION:
: APPLICANT: Koch, Jean-Marc
: APPLICANT: Heichman, Karen
: TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
: FILE REFERENCE: Protein Interactions in ND
: CURRENT APPLICATION NUMBER: US/09/973,077
: PRIOR FILING DATE: 2001-10-10
: PRIOR APPLICATION NUMBER: US 60/240,790
: PRIOR FILING DATE: 2000-10-17
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 4
: LENGTH: 372
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-973-077-4

Query Match          15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2,5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

OY 27 LFFD---LPPASSTDS-----GSGGRLFPD-----LPPASGDSG 60
|||
Db 27 LLODDRVTPTCHSTSEPCRSRFPDGSSPATMDNCGIMDNRIDEPILLPSI----- 81
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OY 61 SLATSIQWVTEGKARKRTSEEEKNGSELEVEKKVCASSVIFGLKGYAERKGEREE 120
|||
Db 82 -----KYG-----KPIKISLENVGASQIGKRK-ENED 109
|||
OY 121 MODAHVILNDITECRPPSSLITRVSYFAVFGHGIGIRASKFAAONLHONLIRKPKGV 180
|||
Db 110 RFD---FAQLTDE-----VLTFVAYDGHGPPAADCHTHMEKCIIMDLPR--- 152
|||
OY 181 ISEKTVKRCLLDTEFKHTDEEFLKQA--SSQKPAWKDGSATATCYLAVDNT-LYIANLGS 237
|||
Db 153 ---EKNLETLTLAFLLEIDKAFSSHARLSADATLLTSGTTATVALRDIELVAVASGDS 209
|||
OY 238 RALICRYNEESOKHAALSLSEKHNPYOYERMRIOKAG-----NVRDGYLVLEVSR 292
|||
Db 210 RALICR-----KGKPMKLTIDHTPERDEKERIKKGGFVAMNSLGGPHNGHLAMTRS 263
|||
OY 293 IGDQYKRCGVTSVPDIRCOL-TPNDRFILLACDGLFKFVTPPEAVNFILSCLEDEKIQ 351
|||
Db 264 IGDIDKTSQVIAEPETRIKRIKHNADSFVLVLTDDGINFMVNSOEICDFVNOCHDPNE-- 321
|||
OY 352 TREKSAADARYEAACNRLANKAVORGSAADVAVVVRIG 391
|||
Db 322 -----AAHAYTEQAIOYGTEDNSTAVVVRIG 347
|||

RESULT 11
US-09-973-063-4
: Sequence 4, Application US/09973063
: Patent No. US20020115119A1
: GENERAL INFORMATION:
: APPLICANT: Koch, Jean-Marc
: APPLICANT: Heichman, Karen
: TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
: FILE REFERENCE: Protein Interactions in ND
: CURRENT APPLICATION NUMBER: US/09/973,063
: PRIOR FILING DATE: 2001-10-10
: PRIOR APPLICATION NUMBER: US 60/240,790
: PRIOR FILING DATE: 2000-10-17
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 4
: LENGTH: 372
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-973-063-4

Query Match          15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2,5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

OY 27 LFFD---LPPASSTDS-----GSGGRLFPD-----LPPASGDSG 60
|||
Db 27 LLODDRVTPTCHSTSEPCRSRFPDGSSPATMDNCGIMDNRIDEPILLPSI----- 81
|||
OY 61 SLATSIQWVTEGKARKRTSEEEKNGSELEVEKKVCASSVIFGLKGYAERKGEREE 120
|||
Db 82 -----KYG-----KPIKISLENVGASQIGKRK-ENED 109
|||
OY 121 MODAHVILNDITECRPPSSLITRVSYFAVFGHGIGIRASKFAAONLHONLIRKPKGV 180
|||
Db 110 RFD---FAQLTDE-----VLTFVAYDGHGPPAADCHTHMEKCIIMDLPR--- 152
|||
OY 181 ISEKTVKRCLLDTEFKHTDEEFLKQA--SSQKPAWKDGSATATCYLAVDNT-LYIANLGS 237
|||
Db 153 ---EKNLETLTLAFLLEIDKAFSSHARLSADATLLTSGTTATVALRDIELVAVASGDS 209
|||
OY 238 RALICRYNEESOKHAALSLSEKHNPYOYERMRIOKAG-----NVRDGYLVLEVSR 292
|||
Db 210 RALICR-----KGKPMKLTIDHTPERDEKERIKKGGFVAMNSLGGPHNGHLAMTRS 263
|||
OY 293 IGDQYKRCGVTSVPDIRCOL-TPNDRFILLACDGLFKFVTPPEAVNFILSCLEDEKIQ 351
|||
Db 264 IGDIDKTSQVIAEPETRIKRIKHNADSFVLVLTDDGINFMVNSOEICDFVNOCHDPNE-- 321
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OY 352 TREKSAADARYEAACNRLANKAVORGSAADVAVVVRIG 391
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Db 322 -----AAHAYTEQAIOYGTEDNSTAVVVRIG 347
|||
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Db 210 RAILCR-----KGRPMKLTIDHTEPRKDEKERIKKCGFVAMNSLIGOPHVNGRLAMTRS 263
Oy 293 IGDGQYKRCGYTVSPDIRCOL-TPNDRFILLACDGLFKVFTPEBAVNFILSCLEDEKIO 351
Db 264 IGDLDLKTSGVIAEPETRIKRIKLHHAHDSFLVLTGGINFMVNSQELCPDVNCHDPNE-- 321
Oy 332 TREGKSADARYEAACNRLANKAVORGSAADVNTVAVVRIG 391
Db 332 -----AAHAVTEDQAIQYGTEDNSTAVVPEFG 347

RESULT 12
US-09-973-964-4
; Sequence 4, Application US/09973964
; Patent No. US20020115606A1
; GENERAL INFORMATION:
; APPLICANT: Roeh, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,964
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-964-4

Query Match 15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2.5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

Oy 27 LIFDD--LPPASSYDS-----GSGGPLLEDD-----LPPASSGDSG 60
Db 27 LQDDRRTVPTCHSSTSEPRCSRPDPDGSFPATWDFGIMDNRIDEPILPSSI----- 81
Oy 61 SLATSIQWVKTGEGARKRTSEEEKNGSEELVEKKVCKASSVITGLGYVAERGEREE 120
Db 82 -----KYG-----KPIPKISLENVGCASQIQKRK-ENED 109
Oy 121 MODAHVILNDITEECRPPSSLITRVSYFAVFDGHCIGIRASKFAAQNLOHNLIRKPKGDV 180
Db 110 RFD-----FAQLTDE-----VLRYAVYDGHGCPAAADCFHHMEKICMDLLPK-- 152
Oy 181 ISVEKTVKRCILDTEFKHTDEEFLKQA--SSQKPAWKDGFATCVLAVDNI-LYIANLGDS 237
Db 153 ---EKNLETLTLALFLEIDKAFSSHARLSADATLLTSGTTATVALLRQIELVAVSGDS 209
Oy 238 RAILCRYNESQKHAALSLSKEHNPTQYEEERMIQKAGS-----NVRDGRVLYGVLEVSRS 292
Db 210 RAILCR-----KGRPMKLTIDHTEPRKDEKERIKKCGFVAMNSLIGOPHVNGRLAMTRS 263
Oy 293 IGDGQYKRCGYTVSPDIRCOL-TPNDRFILLACDGLFKVFTPEBAVNFILSCLEDEKIO 351
Db 264 IGDLDLKTSGVIAEPETRIKRIKLHHAHDSFLVLTGGINFMVNSQELCPDVNCHDPNE-- 321
Oy 332 TREGKSADARYEAACNRLANKAVORGSAADVNTVAVVRIG 391
Db 332 -----AAHAVTEDQAIQYGTEDNSTAVVPEFG 347

RESULT 13
US-09-975-072-4
; Sequence 4, Application US/09975072
; Patent No. US20020115607A1
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; GENERAL INFORMATION:
; APPLICANT: Roeh, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/975,072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-072-4

Query Match 15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2.5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

Oy 27 LIFDD--LPPASSYDS-----GSGGPLLEDD-----LPPASSGDSG 60
Db 27 LQDDRRTVPTCHSSTSEPRCSRPDPDGSFPATWDFGIMDNRIDEPILPSSI----- 81
Oy 61 SLATSIQWVKTGEGARKRTSEEEKNGSEELVEKKVCKASSVITGLGYVAERGEREE 120
Db 82 -----KYG-----KPIPKISLENVGCASQIQKRK-ENED 109
Oy 121 MODAHVILNDITEECRPPSSLITRVSYFAVFDGHCIGIRASKFAAQNLOHNLIRKPKGDV 180
Db 110 RFD-----FAQLTDE-----VLRYAVYDGHGCPAAADCFHHMEKICMDLLPK-- 152
Oy 181 ISVEKTVKRCILDTEFKHTDEEFLKQA--SSQKPAWKDGFATCVLAVDNI-LYIANLGDS 237
Db 153 ---EKNLETLTLALFLEIDKAFSSHARLSADATLLTSGTTATVALLRQIELVAVSGDS 209
Oy 238 RAILCRYNESQKHAALSLSKEHNPTQYEEERMIQKAGS-----NVRDGRVLYGVLEVSRS 292
Db 210 RAILCR-----KGRPMKLTIDHTEPRKDEKERIKKCGFVAMNSLIGOPHVNGRLAMTRS 263
Oy 293 IGDGQYKRCGYTVSPDIRCOL-TPNDRFILLACDGLFKVFTPEBAVNFILSCLEDEKIO 351
Db 264 IGDLDLKTSGVIAEPETRIKRIKLHHAHDSFLVLTGGINFMVNSQELCPDVNCHDPNE-- 321
Oy 332 TREGKSADARYEAACNRLANKAVORGSAADVNTVAVVRIG 391
Db 332 -----AAHAVTEDQAIQYGTEDNSTAVVPEFG 347

RESULT 14
US-09-972-038-4
; Sequence 4, Application US/09972038
; Patent No. US20020119155A1
; GENERAL INFORMATION:
; APPLICANT: Roeh, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,038
; PRIOR FILING DATE: 2000-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
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us-09-935-124a-2.ra1

Page

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:49 : Search time 17 Seconds
(without alignments)
678,458 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018
Sequence: 1 MDLFGDLPERSPPRPAAGK.....KAVRGSSADNVTVVVRICH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	392	4	US-09-013-881-2
2	340	16.8	306	3	US-08-822-701-8
3	340	16.8	306	3	US-08-822-701-8
4	326	16.2	306	4	US-08-822-701-8
5	320.5	15.9	309	2	US-08-822-701-7
6	320.5	15.9	309	2	US-08-822-701-7
7	319	15.8	390	2	US-08-822-701-9
8	319	15.8	390	2	US-08-822-701-9
9	317.5	15.7	281	2	US-08-822-701-9
10	317.5	15.7	281	2	US-08-822-701-9
11	313	15.5	478	3	US-08-873-093-1
12	313	15.5	478	3	US-08-873-093-1
13	313	15.5	479	4	US-08-873-093-4
14	271.5	13.5	314	3	US-08-822-701-10
15	271.5	13.5	314	3	US-08-822-701-10
16	269.5	13.4	392	3	US-08-935-855-22
17	269.5	13.4	392	3	US-08-935-855-22
18	269.5	13.4	542	3	US-08-935-855-20
19	255.5	12.7	546	3	US-08-935-855-20
20	178	8.8	504	2	US-09-144-178-2
21	178	8.8	504	2	US-09-144-178-2
22	178	8.8	504	4	US-09-406-854-2
23	178	8.8	504	4	US-09-529-279-2
24	178	8.8	517	4	US-09-529-279-43
25	178	8.8	517	4	US-09-529-279-11
26	176	8.7	504	2	US-08-752-891-6
27	176	8.7	504	2	US-09-144-178-6

28	176	8.7	504	4	US-09-406-854-6	Sequence 6, Appl1
29	125	6.2	249	4	US-09-134-001C-4777	Sequence 4777, Ap
30	107	5.3	273	4	US-08-320-161-10	Sequence 10, Appl
31	107	5.3	273	4	US-08-455-829-10	Sequence 10, Appl
32	107	5.3	273	4	US-08-235-836C-13	Sequence 13, Appl
33	107	5.3	273	4	US-08-455-873-10	Sequence 10, Appl
34	103	5.1	475	4	US-09-370-838-193	Sequence 193, App
35	100.5	5.0	466	4	US-08-431-836C-107	Sequence 107, App
36	96.5	4.8	1085	2	US-08-938-534-28	Sequence 28, Appl
37	96.5	4.8	1085	2	US-09-345-224-28	Sequence 28, Appl
38	96.5	4.8	1085	4	US-09-916-109-5	Sequence 5, Appl1
39	95	4.7	447	4	US-09-916-109-5	Sequence 4, Appl1
40	95	4.7	483	4	US-09-067-351-3	Sequence 3, Appl1
41	94.5	4.7	422	2	US-09-360-490-3	Sequence 11, Appl
42	94.5	4.7	422	2	US-08-375-709-11	Sequence 11, Appl
43	92.5	4.6	2756	1	US-08-752-929-11	Sequence 7, Appl1
44	92.5	4.6	2756	1	US-09-090-793-7	
45	92.5	4.6	2756	4		

ALIGNMENTS

RESULT 1
US-09-013-881-2
Sequence 2, Application US/09013881
Patent No. 6132964
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purni
TITLE OF INVENTION: HUAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0470 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNO702
CLONE: 195647
US-09-013-881-2

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 6.8e-201;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDLFGDLPEPERSPPRPAKGEAKQKPLFLFDDLPASSSTDGSGGGLFDDLPASSGDSG 60
Db 1 MDLFGDLPEPERSPPRPAKGEAKQKPLFLFDDLPASSSTDGSGGGLFDDLPASSGDSG 60
QY 61 SLATISOMVTEGKAGARKTSEEKNGSEELVEKKVKASSVIGLKGVAERGEREE 120
Db 61 SLATISOMVTEGKAGARKTSEEKNGSEELVEKKVKASSVIGLKGVAERGEREE 120
QY 121 MODAHVILNDITEECRPSLLTRVSYFAVEDGHCIGIRASKRAAQNHLQNLIRKPKGV 180
Db 121 MODAHVILNDITEECRPSLLTRVSYFAVEDGHCIGIRASKRAAQNHLQNLIRKPKGV 180
QY 181 ISVEKTVRCCLDTFKHDEEFLKQASSQKPAKMGSTATCYLVANDNLIYANLDSRAI 240
Db 181 ISVEKTVRCCLDTFKHDEEFLKQASSQKPAKMGSTATCYLVANDNLIYANLDSRAI 240
QY 241 LCRVNEESOKHAALSLSKEHNPTOYEEMRIQKAGNVRDGVLGVLVLSRSIGDGYKR 300
Db 241 LCRVNEESOKHAALSLSKEHNPTOYEEMRIQKAGNVRDGVLGVLVLSRSIGDGYKR 300
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVTPPEAVNFILSCLDEKIQIREGKSAD 360
Db 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVTPPEAVNFILSCLDEKIQIREGKSAD 360
QY 361 ARYEACNRANKAVQSGADNVTWVVRIGH 392
Db 361 ARYEACNRANKAVQSGADNVTWVVRIGH 392
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RESULT 2

US-08-822-701-8
Sequence 8, Application US/08822701
Patent No. 5976853

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
APPLICANT: Basillio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, F1N13
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Rattus

Query Match 16.8%; Score 340; DB 2; Length 306;
Best Local Similarity 33.7%; Pred. No. 6e-27;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

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QY 106 GIKGYAERKGEREMODAHVILNDITEECRPSLLTRVSYFAVEDGHCIGIRASKRAAQ 165
Db 21 GIRYGLSSMOGWRVEMEDAHVAILD-----PSCLTF-WSPFAVYDGHAGSOVAKYCE 73
QY 166 NLHONLIRKFP-KGD--VISVEKTVRCCLDTFKHDEEFLKQASSQKPAKMGSTATCY 222
Db 74 HLHDHITNODFKSGAGAPSE-NYKNGIRGFLBIDHMRVMSKKHAGADRSGSTAVGV 132
QY 223 LAVDNILYIANLGDRAILCRVNEESOKHAALSLSKEHNPTOYEEMRIQKAGNVRDGR 282
Db 133 LISPHOTTFINCGDSRGILCR-----NRKYHFTQDKRPSNPLEKEXIQQNAGSVMIQR 186
QY 283 VLGVLVRSISGDGYKRC---GVT-----SVPDIRRCQLTPNDRFILLACDGLFK 330
Db 187 VNGSLAVSRALGDFYK-CVHGKGFTEQLVSPPEVHDIERSE--EDDQFIILACDGIWD 243
QY 331 VTPPEAVNFILSCLDEKIQIREGKSADARIEACNRANKAVQSGADNVTWVVRIGH 388
Db 244 VMGNEILCDFVRSRLVETD-----LEKVCNEVDYCLYKGRDMSVILI 289
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RESULT 3

US-08-935-855-8
Sequence 8, Application US/08935855
Patent No. 6066485

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
APPLICANT: Basillio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, F1N13
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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Page 3

MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Rattus

Query Match 16.8%; Score 340; DB 3; Length 306;
Best Local Similarity 33.7%; Pred. No. 6e-27;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

OY 106 GLGYAERKGEREMODAHVILNDITEECRPPSLITRVSYFAVFDGHSRASKFAAQ 165
DB 21 GLRYGLSSMOGWRVEMEDAHVAVIGL-----PSGLET-WSEFVAYDGHAGSVAARYCE 73
OY 166 NLHQNLRKFP-KGD--VISVEKTVKRLDLPFKHTDEEFLKQASSQKPAWKDGSTATCV 222
DB 74 HLDHITNNODERGSAGAPSVKNGITGTGLEIDEHMRVSEKRGADRSSTAVGV 132
OY 223 LAVDNILYIANLSDRAILCRYNESQKHAALSKEHNPQYEEHRIQAGAVRQGR 282
DB 133 LISPOHTYFINGDSRGLLGR-----NRRVHEFTQDHPSPLEKERIQAGSVAIQH 186
OY 283 VLGVLEYSRISGDQYKRC---GVY-----SVPIRRCQLTPNDRTILLACGLER 330
DB 187 VNGLAVSRALDQFDYK-CVHGKQPTQLVSPPEVHDENSE--EDQFILLACDQIMD 243
OY 331 VTPPEAVNFIISCLE--DEKIQREKSAADARYACNRLANKAVOGSADNVYMYV 388
DB 244 VMGNEELCDFVRSRLVTD-----LEKVCNEVVDICLKGRSDMMSVIL 289

RESULT 4
US-09-206-646-4
Sequence 4, Application US/09206646
Patent No. 6436637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Lal, Preeti G.
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
FILE REFERENCE: PF-0319
CURRENT APPLICATION NUMBER: US/09/206,646
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ. ID NOS: 4
SOFTWARE: PERL Program
SEQ. ID NO: 4
LENGTH: 390
TOPOLGY: linear
ORGANISM: Homo sapiens
REMARKS:
NAME/KEY: misc feature
OTHER INFORMATION: ID No. 6436637 9452526
US-09-206-646-4

Query Match 15.2%; Score 326; DB 4; Length 390;
Best Local Similarity 30.0%; Pred. No. 2.5e-25;
Matches 98; Conservative 52; Mismatches 121; Indels 56; Gaps 10;

OY 78 KRKTSSEKNGSEELVKKVCASSYIFGLKGYAERKGEREMODAHVILNDITEECRP 137
DB 7 KRKTEKHNHAGN-----GLRYGLSSMOGWRVEMEDAHVAVIGI-----46
OY 138 PSSLITRVSYFAVFDGHSRASKFAAONLHONL-----IRKFPK-GDYI--SVKTYKR 189
DB 47 PHGL-DNMSFFAVYDGHAGSRVANCSTHLEHITTTNEDPRAADKSGSALRPSVE-SVKT 104
OY 190 CLDPTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLSDRAILCRYNESQ 249
DB 105 GRTGTFKIDYEMNFSDLRNGMDRSGSTAVGVMSPTHMVYFINGDSRAVLCRNGQ---161

OY 250 KHAALSKEHNPQYEEHRIQAGAVRQGRVILGVLEYSRISGDQYKRC-----302
DB 162 ---VCFSTQDHPKCPVEKERIQAGSVAIQHNSLAVSRALDQFDYCVGKQPTQ 218
OY 303 -VISVPIRRCQLTPNDRTILLACDGLFKYFTPEEAVNFIISCLEDEKIQREKSAADA 361
DB 219 LVSPPEVEIYRAEDEFVYVACDQIMDMNEELCEFEVSRLE-----VSD 266
OY 362 RYEPACNRLANKAVOGSADNVYMYV 388
DB 267 DLENVCNMYVDICLKGRSDMMSVIL 293

RESULT 5
US-08-822-701-7
Sequence 7, Application US/08822701
Patent No. 5976853
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
NUMBER OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-822-701-7

Query Match 15.9%; Score 320.5; DB 2; Length 309;
Best Local Similarity 29.7%; Pred. No. 6.5e-25;
Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;

OY 78 KRKTSSEKNGSEELVKKVCASSYIFGLKGYAERKGEREMODAHVILNDITEECRP 137
DB 7 KRKTEKHNHAGN-----GLRYGLSSMOGWRVEMEDAHVAVIGI-----46
OY 138 PSSLITRVSYFAVFDGHSRASKFAAONLHONL-----IRKFPK-GDYI--KTV 187
DB 47 PHGL-DNMSFFAVYDGHAGSRVANCSTHLEHITTTNEDPRAADKSGSALRPSVSTGTG 105
OY 188 KRCLDTEKHTDEEFLKQASSQKPAV-KDGSTATCVLAVDNILYIANLSDRAILCRINE 246

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Db      7 KRRTKHNHAGN-----GLRYGLSSMOGMEVEDAHNAVYGI-----46
Oy      138 PSSLTIRVSYFAVFDGHCGRASKFAONLHONL-----IRKPKGDVI---SVKTYKR 189
Db      47 PHLG-EDMSFFAVYDGHAGSRVANYSCTHLEHTTNEDEFAADKSGFALPSVE-NVKT 104
Oy      190 CLDLPFKHTDEEFLKQASSQKPMKDGSTATCVLADVNIILYIANLGDSRAILCRNSESQ 249
Db      105 GIRTGFLKIDEXMRNFSDLNCGMDRSGSTAAGVMISPTHTYFINGDSRAVLGRNGQ---161
Oy      250 KHAALSLSKENHPQYEEBMRKIOKAGNVRDGRVILGVLEYSRSTIGDGVYKRGQ-----302
Db      162 ---VCFSTODHKPCNPMKEKRIQAGSVMIQIRVNGSLAVSRALGDYDTCVDGKGPTEQ 218
Oy      303 -VTSVPDIRCOLTPNDFILLACDGLFVYTPPEAVNFILSCLEDEKIQTRGKSADA 361
Db      219 LVSPEVEYELLRAEEDFEVVLACDGIIMVMSNEELCEFNARLE-----VSD 266
Oy      362 RYEACNRLANKAVRGSAADNVTVMYV 388
Db      267 DLENVCNMVVDTCILHKSGRDMSTIVL 293

RESULT 8
US-09-206-646-3
Sequence 3, Application US/09206646
Patent No. 6436637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti G.
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
FILE REFERENCE: PF-0319-1 DIV
CURRENT APPLICATION NUMBER: US/09/206, 646
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: ID No. 6436637 g247927
US-09-206-646-3

Query Match      15.8%; Score 319; DB 4; Length 390;
Best Local Similarity 29.4%; Pred. No. 1.3e-24;
Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

Oy      78 KRKTSSEKNGSELYBKVCASSVIFGLKGYAEKRGREEMODAHVILNDITECRP 137
Db      7 KRRTKHNHAGN-----GLRYGLSSMOGMEVEDAHNAVYGI-----46
Oy      138 PSSLTIRVSYFAVFDGHCGRASKFAONLHONL-----IRKPKGDVI---SVKTYKR 189
Db      47 PHLG-EDMSFFAVYDGHAGSRVANYSCTHLEHTTNEDEFAADKSGFALPSVE-NVKT 104
Oy      190 CLDLPFKHTDEEFLKQASSQKPMKDGSTATCVLADVNIILYIANLGDSRAILCRNSESQ 249
Db      105 GIRTGFLKIDEXMRNFSDLNCGMDRSGSTAAGVMISPTHTYFINGDSRAVLGRNGQ---161
Oy      250 KHAALSLSKENHPQYEEBMRKIOKAGNVRDGRVILGVLEYSRSTIGDGVYKRGQ-----302
Db      162 ---VCFSTODHKPCNPMKEKRIQAGSVMIQIRVNGSLAVSRALGDYDTCVDGKGPTEQ 218
Oy      303 -VTSVPDIRCOLTPNDFILLACDGLFVYTPPEAVNFILSCLEDEKIQTRGKSADA 361
Db      219 LVSPEVEYELLRAEEDFEVVLACDGIIMVMSNEELCEFNARLE-----VSD 266
Oy      362 RYEACNRLANKAVRGSAADNVTVMYV 388
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Db      267 DLENVCNMVVDTCILHKSGRDMSTIVL 293

RESULT 9
US-08-822-701-9
Sequence 9, Application US/08822701
Patent No. 5976953
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-822-701-9

Query Match      15.7%; Score 317.5; DB 2; Length 281;
Best Local Similarity 31.4%; Pred. No. 1.1e-24;
Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;

Oy      111 VAEKGE--REMODAHVILNDITEBCRPSSLITRV--SYFVDFGHCGRASKFAON 166
Db      23 VAENKSKFRKTMEDVITYKNA-----SRIDMGYAVFDGHCGRIOASWCKKH 72
Oy      167 LH-----ONLIRKPKGDVISEVETKYKCLDTPFKHTDEEFLKQASSQKPMKDGST-ATC 221
Db      73 LHTIITONL-----ADETDVADYLDNSFLAIDET-----NTKLVGNSGTAAYC 119
Oy      222 VL---AVNT-----LYTANGDSRAILCRNSESQKHAALSLSKENHPQY 265
Db      120 VLWELIPSDSDSMIAQHQKLYTANVGDSDRYLFPNGN-----SIRLTYDKHASDT 173
Oy      266 EEBMRKIOKAGNVRDGRVILGVLEYSRSTIGDGVYKRGQ-----SVKTYKR 325
Db      174 LEMQKQAGGGLIKSRVNGMLAVTRSLDRFDSLVYGS-PFTTSVEITSDEKFLILAC 232
Oy      326 DGLFVYTPPEAVNFILSCLEDEKIQTRGKSADARVEACNRLANKAVRGSAADNVTV 385
```

Db 233 DGLMDVIDDQDACELIKIDTEPNE-----AAKVLYRALENGTIDNTV 276

Qy 386 MVV 388

Db 277 MVV 279

RESULT 10

US-08-935-855-9

Sequence 9, Application US/08935855

Patent No. 6066485

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark

APPLICANT: Basilio, Claudio

TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE

TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,855

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-002 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: Saccharomyces cerevisiae

US-08-935-855-9

Query Match 15.7%, Score 317.5, DB 3, Length 281;

Best Local Similarity 31.4%, Pred. No. 1,1e-24;

Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;

Qy 111 VAERGE--REMMDAHYILNDITEECRPSSLITRV--SYFAVNGHGCIASFAAON 166

Db 23 VAENKNSFRRTMEDVHYVKNFA-----SRLDMGYFAVEDGHAGIOASKWCGKH 72

Qy 167 LH---OULIRFPKGDVSYVEKTVKCLLDTFKHTDEEFLKQASSOKPAMWDGST-ATC 221

Db 73 LHTITEQNIL-----ADETRDYRVLANDSFLAIDEI-----NTKLVGNSGCTAAVC 119

Qy 222 VL---AVDNI-----LYIANLGDRAILCRYNESQKHAALSKEHNPTQY 265

Db 120 VLRLWLPDSVSDSDMDLAHQHKKLTYANWGDSRIYLFPRGN-----SIRLLYDHKASDT 173

Qy 266 BERMIAQAGGNVDRGVLGVLEYSRSIGDGQYKRCGYTSVPDIRCOLTPNDRIILLAC 325

Db 174 LEMQAVEQAGGLIMKSRVNGMLAVTRSLGDKFFDSLVVGS--PFTTSVETTSDDKFLIILAC 232

Qy 336 DGLFVETPEEAVNFIILSCLEDEKIQTRREGKSAADARYEAACNRLANKAVRGSDANTV 385

Db 233 DGLMDVIDDQDACELIKIDTEPNE-----AAKVLYRALENGTIDNTV 276

Qy 386 MVV 388

Db 277 MVV 279

RESULT 11

US-08-873-093-1

Sequence 1, Application US/08873093

Patent No. 5853997

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goll, Surya K.

APPLICANT: Lal, Preeti

APPLICANT: Corley, Neil C.

APPLICANT: Zhang, Hong

TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/873,093

FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0319 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 478 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: THPIPL801

CLONE: 131177

US-08-873-093-1

Query Match 15.5%, Score 313, DB 2, Length 478;

Best Local Similarity 28.7%, Pred. No. 7,8e-24;

Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;

Qy 78 KRKTEEEKNGSEELVEKVKACASSVITGLKGYVAERKGEREMODAHYILNDITEECRP 137

Db 7 KRKTEKHNAHNGN-----GLRYGLSSKMGWREMDAHTAVVGI----- 46

Qy 138 PSSLITRVSYFAVFDGHGCIASKEFAAONLHQNLR-----FFPKGDVSYVEKTVK 189

Db 47 PHGL-EDMSFRAVYIGHAGSRVANCSTHLEHTITNEDFRAAGSGSALSLVE-NYKN 104

Qy 190 CLLDTFKHTDEEFLKQASSQKPAWKGSTATCVLAVDNLIYIANLGDRAILCRYNESQ 249

Db 105 GIRTGFLAIDEYMRNFSDLRNGMDRSGSTAVGVMIISPKHITYFINCGDSRAVLYRNGQ--- 161

QY 250 KHAALSLSKENPTOYEERMRIOKAGNVPDGRVLYGLEVSRISICDGYKRCG----- 302
DB 162 ---VCFSTQDHRPCNPREKERIONAGSGVMIORVNGSLAVSRALGDDYDKCYDGGKPTGQ 218
QY 303 -VTSVPDIRRCQLTPNDRFTLLACDGLFVFTPEAVNFILISCLDEKIQTRGKSADA 361
DB 219 LVSPEVEYELIRAEDEFIILACDGIWDMVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEAACNRLANKAVQSGADNVTVMV 388
DB 267 DLENVCNMVVDTCILHKGSRDMSIIV 293

RESULT 12

US-08-873-093-4
; Sequence 4, Application US/0873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goll, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1452526
US-08-873-093-4

Query Match 15.5%; Score 313; DB 2; Length 478;
Best Local Similarity 28.7%; Pred. No. 7.8e-24;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;

QY 78 KRKTSSEKNGSEELVEKKYKCRASSVIFGLKGYAERKGREREMODAHVILNDITEECRP 137
DB 7 KRTEKHNAAGAGN-----GLRYGLSSMQGRVEMEDAHAAVVGI----- 46
QY 138 PSSLTIRVSYFAVPDGHGGRIRASKFAQNLHONLIR-----KPKGDVTSVEKTVKR 189
DB 47 PIGL-EDMSFPAVYDGHAGSRVANCSTHLEHTTTNEDFRAAGKSGSALSLELSE-NVKN 104

QY 190 CLIDTFKHTDEFILKAKSSOKPAMKDGSTANTCVLAVDNILYIANLGRSRAILCRYNESQ 249
DB 105 GIRTGFLKIDEXMRNFSDLRNGMDRSGSTAVGVMSPRHIIYFINGDSRAVLYRRNGQ--- 161
QY 250 KHAALSLSKENPTOYEERMRIOKAGNVPDGRVLYGLEVSRISICDGYKRCG----- 302
DB 162 ---VCFSTQDHRPCNPREKERIONAGSGVMIORVNGSLAVSRALGDDYDKCYDGGKPTGQ 218
QY 303 -VTSVPDIRRCQLTPNDRFTLLACDGLFVFTPEAVNFILISCLDEKIQTRGKSADA 361
DB 219 LVSPEVEYELIRAEDEFIILACDGIWDMVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEAACNRLANKAVQSGADNVTVMV 388
DB 267 DLENVCNMVVDTCILHKGSRDMSIIV 293

RESULT 13

US-09-206-646-1
; Sequence 1, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goll, Surya K.
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; FILE REFERENCE: PF-0319-1.D1V
; CURRENT APPLICATION NUMBER: US/09/206,646
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID NO. 6436637 013177CD1
US-09-206-646-1

Query Match 15.5%; Score 313; DB 4; Length 479;
Best Local Similarity 28.7%; Pred. No. 7.9e-24;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;

QY 78 KRKTSSEKNGSEELVEKKYKCRASSVIFGLKGYAERKGREREMODAHVILNDITEECRP 137
DB 7 KRTEKHNAAGAGN-----GLRYGLSSMQGRVEMEDAHAAVVGI----- 46
QY 138 PSSLTIRVSYFAVPDGHGGRIRASKFAQNLHONLIR-----KPKGDVTSVEKTVKR 189
DB 47 PIGL-EDMSFPAVYDGHAGSRVANCSTHLEHTTTNEDFRAAGKSGSALSLELSE-NVKN 104
QY 190 CLIDTFKHTDEFILKAKSSOKPAMKDGSTANTCVLAVDNILYIANLGRSRAILCRYNESQ 249
DB 105 GIRTGFLKIDEXMRNFSDLRNGMDRSGSTAVGVMSPRHIIYFINGDSRAVLYRRNGQ--- 161
QY 250 KHAALSLSKENPTOYEERMRIOKAGNVPDGRVLYGLEVSRISICDGYKRCG----- 302
DB 162 ---VCFSTQDHRPCNPREKERIONAGSGVMIORVNGSLAVSRALGDDYDKCYDGGKPTGQ 218
QY 303 -VTSVPDIRRCQLTPNDRFTLLACDGLFVFTPEAVNFILISCLDEKIQTRGKSADA 361
DB 219 LVSPEVEYELIRAEDEFIILACDGIWDMVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEAACNRLANKAVQSGADNVTVMV 388
DB 267 DLENVCNMVVDTCILHKGSRDMSIIV 293

RESULT 14

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US-08-822-701-10
: Sequence 10, Application US/08822701
: Patent No. 5976853
: GENERAL INFORMATION:
: APPLICANT: Guthridge, Mark
: APPLICANT: Basilio, Claudio
: TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
: TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/822,701
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1049-1-002 N
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 314 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: ORGANISM: Leishmania
: US-08-822-701-10

Query Match 13.5% Score 271.5; DB 2; Length 314;
Best Local Similarity 28.0%; Pred. No. 8e-20; Indels 83; Gaps 12.
Matches 84; Conservative 43; Mismatches 90;

OY 116 GEREMODAHYLNDITEECRPSSLLITRVSYFAVFDGCHGIRASKAFMAONLHQLIKRF 175
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 31 GYREMEHAHL-----TYLTDSWGFVGFDGHVNQCGOYLEAARSR----- 72

OY 176 PKGVISVEKTVKRCRLDTFKHTDEEFLKQASSQPKMKD-----GSTATCVLAVDN--- 227
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 -----AIKK-----ESIPWTDERMKEELAIRIQEWMDSGREGSGTGFVALKEGNK 119

OY 228 -ILVIANGDSRAILICRNEESQKIHAALSLSKENHPLOYEEEMRIQKAGANRDGVLGV 286
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 VHLQVNGNDSRYVAC-----IDGVCVPLETDHKPNNEGEGRIENCAGRVENNRVDGS 173

OY 287 LEVRSKIDGOYK-----RCGVTSVPDIRCQLT--PNDFFILLACDGLFK-VFTPEE 336
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 174 LAVSAFLCFDDREYKLKGSSGLEKVTALADVQHKDTPFSND-FVLLCCDGVEGKNPNEE 232

OY 337 AVNFLSLDEDEKIQTRRGKSAADARYEAACN-----RLANKAVORCSADNVTVMVVR 389
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 233 VVAAYVKQOLE-----TCNDLAEVAGRVCCEAIEGRSRIINISCMIVQ 273

RESULT 15
US-08-935-855-*0
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: Sequence 10: Application US/08935855
: Patent No. 6066485
:
: GENERAL INFORMATION:
: APPLICANT: Guthridge, Mark
: APPLICANT: Basillico, Claudio
: TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
: TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/935,855
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 314 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: ORGANISM: Leishmania
:
: US-08-935-855-10
:
: Query Match 13.5%; Score 271.5; DB 3; Length 314;
: Best Local Similarity 28.0%; Pred. No. 8e-20;
: Matches 84; Conservative 43; Mismatches 90; Indels 83; Gaps 12.
:
: QY 116 GEREMODAHYTLNDITRECRPSSLIRVSGFAVFDGCGIRASKPAFNAONLHQNLIRKF 175
: | | | | | : : | | | | | : | | | | | : | | | | | :
: Db 31 GYRETMEDAHL-----TYLTDMSGFFGVFDGHVNDQCSYLERARNS----- 72
:
: QY 176 PKGVIVSEVTKVRCLDTPFKHTDEEFLKQASSOKPARKD-----GSTATCVLAVDN-- 227
: : : : : : : : : : : : : : : : : : : : : :
: Db 73 -----AIEK-----ESIPWTDERMKELALRIDQEMNDSGREGSGTGFVALKEGK 119
:
: QY 228 -ILYIANLGDGRALICRNESQKHAALSLEKENPPTOYEEMRIQKAGANNRDRGLVGY 286
: | | | | | : : | | | | | : | | | | | : | | | | | :
: Db 120 VHLGVNGVNDGRVYAC-----IDGVCPLETDHKKPNNEGEGROTIENAGRVENNRVDS 173
:
: QY 287 LEVRSIDQGYK-----RCGVTSVPDIRCOLT--PNDRFILLACDGLPK-VFTPEE 336
: | | | | | : : | | | | | : | | | | | : | | | | | :
: Db 174 LAVSRASCDREYKLGSSQLQKVIALLDVQHKDTPDSND-FVLLCCDGVYEGGNPNEE 232
:
: QY 337 AVNFIISLCEDEKIQTRGKSAADARYEACN-----RLANKAVQKSGADNVTVMYVR 389
: | | | | | : : | | | | | : | | | | | : | | | | | :
: Db 233 VVAIVKQOLE-----TCNDLAEVAGRVCEAFIERGSRDINISCMIVQ 273

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